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Result
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Listing first 45 summaries
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   1837
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Copyright (c) 1993 - 2000 Compugen Ltd
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Claim 43;

Page 78-79; 160pp; English.

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                     (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                           19-JUN-2000; 2000WO-US16915
                                                  18-JUN-1999;
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Chimeric - Borrelia
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                                                                              28-DEC-2000.
                                                                                           W0200078966-A1
                                                                                                                  Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick
                                                                                                                                   Borrelia sp chimeric ospC protein SEQ ID NO: 60.
                                                                                                                                                       03-APR-2001 (first entry)
                                                                                                                                                                                                   2728
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Best Local
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les 374; Conservative
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        Dykhuizen D,
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Pred. No. 3.2e-119;
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Gomes-Solecki M;
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18-JUN-1999;

9908-0140042

19-JUN-2000; 2000WO-US16915

28-DEC-2000 WO200078966-A1.

Chimeric - Borrelia sp. Chimeric - Borrelia sp.

Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick.

Borrelia sp chimeric ospC protein SEQ ID NO:

(first entry)

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                           Claim 43; Page 123; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
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DB; AAF29032.
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73; Conservative
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Pred. No. 5.6e-119;
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RESULT
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(BROO-)
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               Chimeric - Chimeric -
                                      Borrelia; ospC;
                                                                      03-APR-2001
                                                                                                    AAB62712
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                                                      Borrelia
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DB; AAF29042.
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                                                      sp chimeric
                                                                                                    standard;
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               Borrelia
Borrelia
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98.7%;
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Pred. No. 5.6e-118;
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                                      protein; tick.
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                                                                        AAB62711 standard;
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98.1%;
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detect immune
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Borrelia 03-APR-2001

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AAB62729 standard;
                                                                           361 AAKEMLTNSVKEL 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 43; Page 81; 160pp; English.
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Lyme disease are used
to Lyme disease -
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Chimeric - Borrelia
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                                                                                                                                                                                                                                                                                                                                                                Local Similarity les 327; Conserv
                                                                                                                                                                                                                                                                                                             Borrelia; ospC; Lyme
                                                                                                         KAKKCSBEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSK 360
                                                                                                                                                             TSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIE
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DB; AAF29015.
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                      Protein;
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87.7%; Pred. No. 2.4e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides from strains of Borrelia which cause
d to immunize animals and detect immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease; vaccine; chimeric protein; tick.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
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Best Local
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                                                                                                             205 ltspvvaespamvnnsgkdgntsansadesvkgpnlteiskkitesnavvlavkeietll
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Lyme disease are used
to Lyme disease -
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Chimeric -
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mes 326; Conserv
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aakemlansvkel
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Borrelia
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Pred. No. 4.2e-102;
1; Mismatches 25;
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Chimeric -
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Lyme disease are used
to Lyme disease -
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298
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DB; AAF29043.
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Pred. No. 4.3e-101;
22; Mismatches 25;
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Matches 324; Conserv
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N-PSDB; AAF29017.
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                                                                                                                                                                                                                                                                                         to Lyme disease
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385 lakaakemlansvkel 400
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Borrelia
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                                                                                                                                                85.0%; Score 1566; DB 22;
85.9%; Pred. No. 1.7e-100;
tive 22; Mismatches 27;
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Best Local
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(BROO-)
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Chimeric - Borrelia
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                                                                                                                                                      to Lyme disease.
                                                                                                                                                                                                           Claim 43; Page 91-92;
                                                                                                                                                                                                                                                                                        Dattwyler RJ,
121 KLKEKHTDLGKEGYTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANSV
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                          GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFTN 120
                                                            ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI
                gkkikndgsldneanrnesllagaytistlitqklsklngseglkekiaaakkcseefst
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                                                                                                                                                                                                                                                                                      Dykhuizen D,
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25

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Similarity 86.7 26; Conservative

10;

Score 1526; DB 22; Pred. No. 1e-97; 0; Mismatches 32;

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to Lyme d
                       The present invention provides compositions comprising ospc protein chimeric ospC proteins from members of the Borrelia genus. These members of the Borrelia genus. These can be used Borrelia burgdorferi, B. afzelii or B. garinii. These can be used vaccines against Borrelia infection, which is spread by ticks and
Sequence
                                                                                                                                                                        (UYNY )
(BROO-)
                                                                      Claim 43; Page 128-129; 160pp;
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                                                                                           Compositions of OspC |
Lyme disease are used to Lyme disease -
                                                                                                                             N-PSDB;
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Borrelia
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                                                                                                polypeptides from strains of Borrelia which cause d to immunize animals and detect immune responses
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                                                                                                                                                                               Claim 43; Page 99-100;
                                                                                                                                                                                                                                            Compositions of OspC |
Lyme disease are used
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                                                            The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzeli or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
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Query Match

81

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Score 1493;

ВB

22;

Length 368;

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea

be

Claim 43; Page 112-113; 160pp;

English

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2; Mismatches 34;
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Best Local S
Matches 313
   Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                   WPI; 2001-050113/06.
N-PSDB; AAF29038.
                                                                                                                                                               Chimeric - 1
Chimeric - 1
                                                           Dattwyler RJ,
                                                                                                              19-JUN-2000; 2000WO-US16915
                                                                      (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                                                 18-JUN-1999;
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                                                                                                                                                                               Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick.
                                                                                                                                                                                               Borrelia sp chimeric ospC protein SEQ ID NO:
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                                                                                                                                                                                                                                     AAB62734;
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Borrelia
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Pred. No. 3.6e-95;
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                                                       Luft
                                                      ВJ,
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            Borrelia which cause
                                                    Gomes-Solecki M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia sp chimeric ospC protein SEQ ID NO:
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11; Conservative
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Borrelia
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Pred. No. 3.1e-95;
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                              Gomes-Solecki
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Lyme disease are used
                                                                           Chimeric -
Chimeric -
                                                                                                      Borrelia;
                                                                                                                     Borrelia sp
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                        19-JUN-2000;
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                                                                                                                                                                          AAB62737 standard;
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                                                                           Borrelia
Borrelia
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       99US-0140042
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                                                                                                                     ospc
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                                                                                                                                                                                                                                                                                                                        The present invention provides compositions comprising ospC prechimeric ospC proteins from members of the Borrelia genus. The Borrelia burgdorferi, B. afzelli or B. garinii. These can be u vaccines against Borrelia infection, which is spread by ticks
                                                                                                                                                                                                                                                                                                                                                                                        Compositions of OspC |
Lyme disease are used
to Lyme disease -
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Search completed: March 18, 2002, 09:54:29 Job time: 327 sec

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OM protein - protein search, using sw model
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

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Copyright (c) 1993 - 2000 Comp
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US-08-235-836C-122
US-08-235-836C-107
US-08-158-353-2
US-08-158-353-2
US-08-158-353-4
US-08-235-836C-34
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US-08-328-254-6
US-08-353-700-1
PCT-US95-16216-1
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US-08-605-958-2
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RESULT 2
US-08-235-836C-30
Sequence 30, App
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                             NAME: BOGOSIAN, MARGATET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BITTELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                       TOPOLOGY: lir
MOLECULE TYPE:
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MARGARET C.
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor NUMBER OF SEQUENCES: 144
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APPLICANT: Luft, Benjamin J.
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                                                                                                LENGTH: 210 amino
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT APPLICATION UNMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-06-13
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SEQ ID NO 15
LENGTH: 209
TYPE: PRT
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APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, E:
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                                                                 KLKEKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                     IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5, Application US/09196293 6183755
                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                          50.4%;
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98.4%;
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                                                                                                                                                                                                                                                                                    Score 928; DB 4;
Pred. No. 9.5e-60;
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Pred. No. 4.9e-60;
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                                                                                                                                                                                                                                                                                                         Length 209
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Patent No.

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                                                                            RESULT 5
US-08-235-836C-122
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US-08-158-353-3
                                                                                                                                     용
                 Sequence 122, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION:
APPLICANT: Dunn, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08158353 Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Carroll, Alice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Milit
CITY: Lexington
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Padula, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                        197
                                                                                                                                                                   181 ELTSPVVAESP 191
                                                                                                                                                                                                137
                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                              1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                                                                                                                             KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                     ELTSPVVAESP 207
                                                                                                                                                                                                                                                                                                                                                                             188;
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Dunn, John J.
Luft, Benjamin J.
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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Methods for Diagnosing Early Lyme
                                                                                                                                                                                                                                                                                                                                                                                         50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 928; DB 1; Length 210; Pred. No. 9.5e-60;
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                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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US-08-209-603E-15
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                                                                                                                                                       Sequence 15, Application US/08209603E Patent No. 6248538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C
                                                                                                                                            GENERAL INFORMATION:
                                                APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-MURSIC, VE
APPLICANT: MOTZ, MANERED
APPLICANT: SOUTSCHECK, ERNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NO TITLE OF INVENTION: BO NUMBER OF SEQUENCES: 1-CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: BN TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1:
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LENGTH: 588 amino acids
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                                                                                                                                                                                                                                                                   466 SPVVAESPKKPGTMAQYNQMHMLSNKSASQNVRTAEE 502
                                                                                                                                                                                                                                                                                                                                      346 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 SPVVAESP-----AMVNN----SGKDGNTSANSADE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 KIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Pred. No. 4.3e-59;
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RESULT 7
US-08-235-836C-107
; Sequence 107, Application US/08235836C
; Patent No. 6248562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REALABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS VERSION 6.2

SOFTWARE: ASCII
CURRENT APPLICATION DATA:
ADDITICATION NUMBER: US/08/209,603E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIF N/A

HYPOTHETICAL: N/A

""T-SENSE: N/A

""DE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEPAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
FILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
                                                                                             197 ELTSPVVAESP 207
                                                                                                                          181 ELTSPVVAESP 191
                                                                                                                                                       121 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGABELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: amit PUBLICATION INFORMATION: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: DSM 5662
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                              61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                          17 ISCNNSGKOGNTSANSADESVKGPNLTEISKKITDSNAVILAVLEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DALL. 436
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/02282
APPLICATION NUMBER: PCT/EP90/02282
TMC DATE: 21_DEC-1990
TMC DATE: 75.07/862,535
                                                                                                                                                                                                                                                                            1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                       KLKEKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLEESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                                IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETN 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BROC
STREET: 99 PARK
CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid analysis
                                                                                                                                                                                                                                                                                                                                           Score 921; DB 4
Pred. No. 3e-59;
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 210;
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US-08-158-353-2
                    GENERAL INFORMATION:
APPLICANT: Padula, Steve
TITLE OF INVENTION: Meth
TITLE OF INVENTION: Disc
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                           Sequence 2, Application US/08158353
Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-836C-107
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    456 SPVVAESP 463
                                                                                                                                                                                                                                 184 SPVVAESP 191
                                                                                                                                                                                                                                                            124 EKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
              ADDRESSEE:
                                                                                                                                                                                                                                              396 AKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 455
                                                                                                                                                                                                                                                                                                        336 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNKLK
                                                                                                                                                                                                                                                                                                                                                              NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      64 KIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 98.98; es 186; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
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CITY: Upton
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 466 amino acids amino acid
    Hamilton, Brook,
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                                                                              Steven J.
                                                   Methods for
Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 915; DB 4;
Pred. No. 2.3e-58;
0; Mismatches 2
Smith & Reynolds, P.C
                                                    Diagnosing Early Lyme
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STREET: CITY: L STATE:

Lexington

Two Militia Drive

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                                                                                                                                                                                                                                                                            Sequence 2, Application US/08031295 Patent No. 5530103
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Best Local S
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TELEFAX: 617-861-9540
NFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W.,
CITY: Washington, D.C.
                                                                                                                                                                                 APPLICANT: LIVEY, IAN
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                             178
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FILING DATE:
CLASSIFICATION: 435
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nes 145; Conserv
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                                                                                                COUNTRY:
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Patentin Release #1.0,
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74.7%; Pred. No. 1.2e-41;
14. Mismatches 27;
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                                                                                                                                Suite 500
 Version #1.25
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US-07-903-580-2
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/903,580
FILING DATE: 25-JUN-1992
PRIOR APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 212 amino acids
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                               APPLICANT: LIVEY, Ian APPLICANT: DORNER, Freidrich
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                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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TELEFAX: \___
TEX: 904136
                                                                                                                                ADDRESSEE: Foley of STREET: 1800 Diagon CITY: Alexandria STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/727,245 FILING DATE: 11-JUL-1991
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                                                                                               ZIP:
                                                                                                              COUNTRY:
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                                                                                               22313-0299
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                                                                                                              Virginia
Y: USA
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                                                                                                                                                                   E: Foley & Lardner
1800 Diagonal Road,
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PatentIn Release #1.0,
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73.68;
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Pred. No. 1.5e-40;
                                                                                                                                                                      Suite
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 Version #1.25
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 19920

US/07/903,580

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CONTROL TYPE: US-07-903-580-2
                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08158353 Patent No. 5620862 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                       08-158-353-4
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 300 TELECOMMUNICATION INFORMATION: TELEPHONE: (702)836-3300
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APPLICATION NUMBER: US 07/727,245
FILING DATE: 11-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
CLASSIFICATION: 435
                         APPLICATION NUMBER: US/08/158,353
                                                                                                                                                             COUNTRY:
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APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
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                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                             Steven J.
Methods for Diagnosing Early Lyme
                                                                                                                                                                                                                                                                      Disease
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73.6%;
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Pred. No. 1.5e-40;
14; Mismatches 35
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                                                                                                                                                                                                                  Smith & Reynolds, P.C.
                                                         Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 212;
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; ORGANISM: Borrelia burgdorferi
US-09-196-293-11
                                                                                                                                                           APPLICANT: MOLES, NORTHER
APPLICANT: MOLES, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
FIILE REFERENCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1990-12-12
EARLIER FILING DATE: 1990-12-22
EARLIER APPLICATION NUMBER: DE DE 39 42 728.5
EARLIER APPLICATION NUMBER: DE DE 39 42 728.5
EARLIER APPLICATION NUMBER: DE DE 39 42 728.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                         SEQ ID NO 11
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: US-08-158-353-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 61/-001 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11,
                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                        EARLIER APPLICATION NUMBER: DE P40 18 988.0 EARLIER FILING DATE: 1990-06-13 NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fuchs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 VKELTSPVVAESP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 VKELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AIGKKIHONNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1, Application US/09196293 6183755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll, Alice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Renate
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; Pred. No. 3.5e-37;
14; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UCT93-05
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Best Local Similarity 70.9 Matches 136; Conservative

70.5%;

Pred. No. 4.8e-37; 2; Mismatches 43

43;

Indels

2

Gaps

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1 MACNNSGKDG-NTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAK 59

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                                                                                                                                                                                                       TELEFONMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 11:
                 HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
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                                                                                                   TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE FROM BORRELIA BURGDORFERI INUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
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                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                          DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUCHS, RENATE WILSKE, BETTINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTZ, MANFRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREAC-MURSIC, VERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS-DOS Version 6.2
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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-209-603E-11
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Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34,
          TELEFAX: (516) 282-372
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
                                                                                  NAME: Bogosian, Margaret C.
REGISTATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                   APPLICATION NUMBER: US 01
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 VKELTSPVVAESP 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
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                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY:
                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Brookhaven National Laboratory
   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08235836C
212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                       516)
                                                                                                                                                                                                                                            29-APR-1994
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                                                    282-3729
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70.5%;
                                                                      282-7338
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Borrelia Polypeptides and Uses 7
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                                                                                                                                                                                            US 08/148,191
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; MOLECULE TYPE: US-08-235-836C-34

protein

Length 212;

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TOPOLOGY: linear

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-836C-32
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                Query Match
Best Local Similarity
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Patent No. 6248562
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                                                                                                                                                                       TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION IMPORMATION:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSian, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VKELTSPVVAESP 191
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197 VKELTSPVVAESP 209
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                                                                                                                                                                                                                                                                                                            NAME: Bogosian, Margaret C
REGISTRATION NUMBER: 25,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKENLANS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Brookhaven National Laboratory
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                  32.6%;
68.2%;
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              Score 600.5; DB 4; Pred. No. 3.2e-36;
                                Length 209;
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             180 KELTSPVVAESP 191
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                                                   NKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSV 179
                                                                               IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFT 119
                                                                                                                       SCNNSG--GDTASTNPDESAKGPNLTVISKKITDSNAFVLAVKEVEALISSIDELANKA 74
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Search completed: March 18, Job time: 345 sec 2002, 09:55:32

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Sequence:
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Gapop 10.0 ,
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/cgn2_6/ptodata/2/paa/US06_(
/cgn2_6/ptodata/2/paa/US07_(
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US-09-596-746A-28
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ALIGNMENTS

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205.	209.	209.	212.	213.	213.	217.	245.	245.	1248.5	253.	281.	281.	284.	289.	48	48	48	49	49	49	49	49	49	49	52	52	52	53	56	95	57	157	9	589.	592.
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-09-596-74	-09-596-746A-	-09-596-746-6	-09-596-746-3	-09-596-746A-	-09-596-746-5	-09-596-746A-	-09-596-746A-7	-09-596-746-7	US-09-596-746-42	-09-596-746A-	-09-596-746A-6	-09-596-746-6	-09-596-746-3	-09-596-746A-	-09-596-746A-7	-09-596-746-7	-09-596-746-5	-09-596-746A-	-09-596-746-7	-09-596-746A-	-09-596-746-5	-09-596-746A-	-09-596-746-4	-09-596-746A-4	-09-596-746A-	-09-596-746-6	-09-596-746-3	-09-596-746A-3	-09-596-746A-	-09-596-746-30	-09-596-746A-	-09-596-746-82	-09-596-746A-	-09-596-746-6	-09-596-746-2
equence 70, App	equence 68, App	equence 68, App	equence 32, App	equence 54,	equence 54, App	equence 32, App	equence 74,	equence 74,	uence 42,	equence 42, App	equence 66, App	equence 66, App	equence 36, App	equence 36,	equence 78, App	equence 78, App	equence 56, App	equence 72, App	equence 72, App	equence 52, App	equence 52, App	equence 56, App	equence 40, App	equence 40, App	equence 64,	equence 64, App	equence 34, App	equence 34, App	equence 30, App	equence 30, App	equence 82, App	equence 82, App	equence 62, App	equence 62,	equence 26, App

US-09-596-746A-24; Sequence 24, Application US/09596746A; GENERAL INFORMATION: ; OTHER INFORMATION: OSPC Chimera US-09-596-746A-24 RESULT NUMBER OF SEQ ID NOS: 84 SOFTMARE: FastSEQ for Windows Version 4.0 SEQ ID NO 24 LENGTH: 375 TYPE: PRT ORGANISM: Artificial Sequence APPLICANT: Dykhuizen, Danial APPLICANT: Luft, Benjamin J. APPLICANT: Maria J.C. Gomes Solecki TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di FILE REFERENCE: 2631.1002-001 CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-06-18 APPLICANT: FEATURE: Dattwyler, Raymond J. Seinost, Gerald Disease in Humans

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1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60

Query Match
Best Local Similarity
Matches 375; Conserv

Conservative

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Score 1842; DB 19; Pred. No. 8.8e-125; Mismatches 0;

Indels Length 375;

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Gaps

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APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
FILE REFERENCE: 2631.002-001
CURRENT APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR FILING DATE: 1999-06-18
NUMBER: US/09/596,746
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Matches 374; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
Q ID NO 24
LENGTH: 374
TYPE: PRT
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182 LTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLL
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                                                        122 LKEKHTDLGKEGVTDADAKEAILKTNGTKTKGABELGKLFESVEVLSKAAKEMLANSVKE 181
                                                                                                              62 GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNK 121
                                                                                                  61 GKKIHONNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNK
                                                                                                                                                                      2 ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 61
                                          LKEKHTDLGKEGVTDADAKEATLKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AAKEMLTNSVKELTS 375
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                                                                                                                                                                                                                   99.7%; Score 1837; DB 19
100.0%; Pred. No. 2e-124;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                DB 19;
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APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: Groups of Borrelia burgdorferi and FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
PRIOR FILING DATE: 1999-06-18
SOFTWARE: PRAFERO 6.
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US-09-596-746-60
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Best Local Similarity
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                              362 AKEMLTNSVKELTS
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                                                    AKKĆŚEEFTAKLKGEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKA
                                                                                                         TSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEK
                                                                                                                     TSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEK 301
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             398
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APPLICANY: Dattwyler, Raymond J.

APPLICANY: Seinost, Gerald

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki

TITIE OF INVENTION: Groups of Borrelia burgdorferi and

TITIE OF INVENTION: Borrelia afzeili That Cause Lyme Disease in Huma

FILE REFERENCE: 2631.1002-001

CURRENT APPLICATION NUMBER: US/09/596,746A

CURRENT FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84
APPLICANT: Selnost, Gerald

APPLICANT: Dykhuizen, Danial

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki

TITLE OF INVENTION: Groups of Borrelia burgdorferi and

TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans

FILE REFERENCE: 2631.1002-001

CURRENT APPLICATION NUMBER: US/09/596,746

CURRENT FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/140,042
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Sequence 60, Application US/09596746A

GENERAL INFORMATION:
                                                                                                                                                                                                                                    RESULT 5
US-09-596-746-80
Sequence 80, Application US/09596746
GENERAL INFORMATION:
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SEQ ID NO 60
LENGTH: 399
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Matches
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APPLICANT:
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ORGANISM: OSPC Chimera
09-596-746A-60
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99.7%;
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Pred. No. 3.6e-124;
1; Mismatches 0;
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ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 61

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: Sequence 80, Application US/09596746A

: GENERAL INFORMATION:
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SEQ ID NO 80
LENGTH: 401
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 Query Match
Best Local Similarity
Matches 372; Conserv
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Best Local Similarity
                                                                                                                                               APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Goroups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US-09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US-60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
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NUMBER OF SEQ ID NOS:
                                                                                    LENGTH: 402
TYPE: PRT
ORGANISM: ospC Chimera
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             98.8%;
98.7%;
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Score 1819.5; DB 19 Pred. No. 4.1e-123; 2; Mismatches 0;
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; OTHER INFORMATION: OspC Chimera US-09-596-746-28
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
                                                                                                                                                                                                           Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
RIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                           TYPE: PRT
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NUMBER OF SEQ ID NOS: 84
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 ELTSPVVAES---PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV
                                      KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                      IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                         MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA
                                                                                                                                                       MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                       IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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Maria J.C. Gomes-
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                                                                                                                                                                                            98.3%;
nilarity 98.1%;
Conservative
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                                                                                                                                                                                         Score 1810.5; DB 19; Length Pred. No. 1.7e-122; 2; Mismatches 2; Indels
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Best Local
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LSKAAKEMLTNSVKELTS
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; OTHER INFORMATION: OSPC Chimera US-09-596-746A-28
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 28
LENGTH: 378
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APPLICANT: Luit, Benjamin J
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi
TITLE OF INVENTION: Borrelia afzelii That Cause Lym
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 050/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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LSKAAKEMLTNSVKELTS 375
                                                          EIEKAKKCSEEFTAKLKGEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESYKN
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98.1%;
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Pred. No. 1.7e-122;
2; Mismatches 2; ]
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US-09-596-746A-26

Sequence 26, Applica GENERAL INFORMATION:

Application US/09596746A

APPLICANT:

Dattwyler, Raymond J.

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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Dises
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 26, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
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Best Local Similarity
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APPLICANT: Maria J.C. Gomes-Solecki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.7%; Score 1597.5; DB 1
87.7%; Pred. No. 4.3e-107;
Live 20; Mismatches 25;
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        in Humans
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4 0
SEQ ID NO 26
LENCTUP. 7-7
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; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746-62
                                            SOFTWARE: Fa
SEQ ID NO 62
LENGTH: 397
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                     APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia bur
TITLE OF INVENTION: Borrelia afzelii That
                                                                                           FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 373
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                               FastSEQ
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87.7%;
                                                                                 Windows Version
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Query Match Best Local :

Local Similarity

86.3%;

Score 1589.5; DB 1 Pred. No. 1.8e-106;

DB 19;

Length

397;

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; ORGANISM: OSPC
US-09-596-746A-62
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                                                                                                                                                                                                                                                              SEQ ID NO 62
LENGTH: 398
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Best Local
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Groups of Borrelia burgdorferi
TITLE OF INVENTION: Borrelia afzelii That Cause Lyn
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                       GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
                                                                                                            ACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 61
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                                                                                              SCHNSGKDGHTSANSADESVKGPHLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 85
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                                                                                                                                                  Score 1589.5; DB 19 Pred. No. 1.8e-106; 1; Mismatches 25;
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US-09-596-746-82
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US-09-596-746-82
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SEQ ID NO 82
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APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi an
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
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TYPE: PRT
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                             GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
                                                                                             TLLASIDELATKAIGKKIQONGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKE 324
                                                                                                                                                                        LTSPVVAES---PAMYNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 238
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                                                                                                                          TLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA 297
                                                                                                                                                                                                                                                                                                                                                  SCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 84
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: Sequence 82, Application US/09596746A 

: GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows VG
SEQ ID NO 82
LENGTH: 401
TYPE: PRT
                                                                                                                                       Sequence 30, Application US/09596746 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
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Seinost, Gerald
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86.4%; Pred. No. 2e-105;
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        Disease
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; FILE REFERENCE: 2631.1002-001
; CURRENT APPLICATION NUMBER: US/09/596,746
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/140,042
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OspC Chimera
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Search completed: March 18, 2002, 10:08:42 Job time: 970 sec

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Compugen Ltd

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Result
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	KTKGABELGKLFESVEVLSKAAKEMLANS 	LK-NI	KKITDSNAVLLAVKEVEALLSS)B 6; .39; 31;	Hn.		-5835 -12996 -12996 -12996 -21160 -2160 -2160 -2160 -2160 -2160 -2160 -2160 -2160 -216
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	EVLSI ESLSI	NEGLKEKIDAAKKC : SEGLKEKIAAAKKC	EALI	Lengt Indel	nts		
	KAA H	AAK	155	.h 21			seque seq seq seq seq seq seq seq seq seq se
	SKAAKEMLANS SKAAKEMLANS	KCSETF	'EALLSSIDEIAAKA : EALLSSIDEL-AKA	11;			
	ANS	ETFT :	AKA AKA	G			
	178 195	119 135	60 75	sdt			5835, 12996, 12996, 21161, 21160, 21159, 21159, 33, App 63, App, 63, App, 64, App, 65, App, 66, App, 66, App, 66, App,
				ω			35, Ap 396, A 160, A

Sequence 7, Application US/09974992 GENERAL INFORMATION:

APPLICANT: Mathiesen, Marianne J. APPLICANT: Theisen, Michael

Holm, Arne

APPLICANT:

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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VGT. 2.1
SEQ ID NO 7
LENGTH: 212
TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-974-992-7
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US-09-974-992-3
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         Query Match
Best Local Similarity
Matches 127; Conserv
                                                                                                                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 3
LENGTH: 207
                                                                                               ORGANISM: Borrelia garinii -09-974-992-3
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                           APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.3%;
Best Local Similarity 69.9%;
Matches 135; Conservative 1
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Holm, Arne
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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INERAL INFORMATION:
APPLICANT: Mathiesen, Marianne J.
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TITLE OF INVENTION: Novel OspC-derived peptide
FILE RFERENCE: 459-666P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 VKELTSPVVAESP 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09974992
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       31.9%;
ilarity 66.5%;
Conservative 2
         24;
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   Score 587.5; DB 6;
Pred. No. 2.2e-33;
24; Mismatches 37;
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Pred. No. 3.4e-35;
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
COATION: 1..1014
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1014
COTHER INFORMATION: Ceres Seq. ID 1836847
US-09-708-427-19883
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US-09-708-427-19883
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Matches 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID FILE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19883
LENGTH: DE 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19883, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
695
                                                                                                      236
                                                                                                                                                                                                        575 RDLEGKIKSYEEQLAEASGKSSSLKEKLEQTIGRLAAAESVNEKLKQEFDQAQEKSLQSS 634
                                                                                                                                                                                                                                            127 TDL-GKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP 185
                                                                                                                                                                                                                                                                                  517 AEESLEQKG--REIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKL 574
                                                                                                                                                                                                                                                                                                                                                          461 LEA---TVDEYSVKISESENLLESIRNELNVTQG-KLESIENDLKAAGLQESEVMEKLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                    401 KHGETEADSKGYLGQVAELQSTLEAFQVKSSSLEAALNIATENEKELTENLNAVTSEKKK 460
                                                                                                                                                                                                                                                                                                                      95 KLDGLKNEGLKEKIDAA-----LKEKH 126
                                                                                                                                                                                                                                                                                                                                                                                              46 VEALLSSIDEIAAK------AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTL--IKQ 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                        THENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKESGDLAE
                                                                                                                                SESELLAETNNOLKIKIQELEGLIGSGSVEKETALKRLEEAIERFNOKETESSDLVEKLK 694
                                                                                                                                                                  VVAESPAMVNNSGK-----DGNTSANSADESVKGPNLTE----ISKKITESNAVVLAVK 235
                                                                                                  EVETLLTSIDELA-KAIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDGNTSANSADE------SVKGPNL-----TEISKKITDS-NAVLLAVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%; Score 175; DB 6; 24.3%; Pred. No. 0.00039;
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372

-ELTS 375

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: NAME/KEY: misc_feature
: LOCATION: 1..1018
: OTHER INFORMATION: Xaa is a
: NAME/KEY: misc_feature
: LOCATION: 1..1018
: OTHER INFORMATION: Ceres Se
US-09-708-427-19882
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US-09-708-427-19882
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION ON 1005: 85364
SOPTWARE: Patentin version 3.1
SEQ ID NOS: 84364
SOPTWARE: Patentin version 3.1
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Best Local Similarity
Matches 118; Conserv
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812
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                                                                                                                                                                                                                                                                                                                                                                                                                                          95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 KDGNTSANSADE-----SVKGPNL-----TEISKKITDS-NAVLLAVKE 45
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                                                                                                                                                                                                                                                                                                                                                                                                AEESLEQKG - - REIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                        KLDGLKNEGLKEKIDAA - - - - -
                               KGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK-NLSKAAKEMLTNSVK- 371
                                                                                                                                                         THENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKESGDLAE
                                                                                                                                                                                              EVETLLTSIDELA-KAIG------KKIKN----
                                                                                                                                                                                                                                   SESELLAETHNQLKIKIQELEGLIGSGSVEKETALKRLEEAIERFNQKETESSDLVEKLK
                                                                                                                                                                                                                                                                                                                  RDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAESVNEKLKQEFDQAQEKSLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEA---TVDEYSVKISESENLLESIRNELNVTQG-KLESIENDLKAAGLQESEVMEKLKS
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                                                                                                             -DVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-EIEKAKKCSEEFTAKL--
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EGEKLQSQIEKLRAVAAEKSVLESH---
                                                                          VNLKLNLELANHGS-----EANELQTKLSALEAEKEQTANELEASKTTIEDLTKQLTS
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Pred. No. 0.0004;
0; Mismatches 161; Indels 136;
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- FEELEKTLSEVKAQLKENVENAATASVKV
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; LOCATION: 1..1269
; OTHER INFORMATION: Xaa is ;
; NAME/KEY: misc_feature
; LOCATION: 1..1269
; OTHER INFORMATION: Ceres S:
US-09-708-427-19881
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US-09-708-427-19881
; Sequence 19881, Application US/09708427
; GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19881
LENGTH: 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 118; Conservative
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Best Local Similarity
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Arabidopsis thaliana
1117
                                                                                    1063
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                                 372 -ELTS 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 AELTS 870
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                                                                                                                                                                                                                                                                                                                                                                                                                               RDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAESVNEKLKQEFDQAQEKSLQSS 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEESLEQKG--REIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKL 829
    AELTS 1121
                                                                                    EGEKLQSQIEKLRAVAAEKSVLESH-----FEELEKTLSEVKAQLKENVENAATASVKV 1116
                                                                                                                                                                      VNLKLNLELANHGS-----EANELQTKLSALEAEKEQTANELEASKTTIEDLTKQLTS 1062
                                                                                                                                                                                                                                                                                                                                             SESELLAETNNQLKIKIQELEGLIGSGSVEKETALKRLEEAIERFNQKETESSDLVEKLK 949
                                                                                                                                                                                                                                                                                                                                                                                    VVAESPAMVNNSGK-----DGNTSANSADESVKGPNLTE----ISKKITESNAVVLAVK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDL-GKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEA---TVDEYSVKISESENLLESIRNELNVTQG-KLESIENDLKAAGLQESEVMEKLKS 771
                                                                                                                          KGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK-NLSKAAKEMLTNSVK- 371
                                                                                                                                                                                                            -DVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-EIEKAKKCSEEFTAKL-- 313
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RESULT

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RESULT 8
US-10-032-585-7646
Sequence 7646, Application US/10032585
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I FEATURE:

NAME/KEY: misc_feature
LOCATION: 1..1313
OTHER INFORMATION: Xaa is any amino acid
LOCATION: 1.1313
LOCATION: 1.1313
OTHER INFORMATION: Ceres Seq. ID 1828627
US-09-708-427-15044
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Best Local Similarity 22.2
Matches 118; Conservative
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243B
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 15044
LENGTH: 1313
TYPE: PRT
                                                                                                                                                                                  439 SEAKATLLVCQEELKNC---ESQVDSLKLASKETNEKYEKMLEDARNEIDS
                                                                                                                                                                                                               329 NAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKE----MITNSVKELTS 375
                                                                                                                                                                                                                                               Sequence 15044, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                334 ELLEKTIEAQRTDLEEYGRQVCIAKEÉASKLENLVESIKSELEISQEEKTRALDNEKAAT 393
                                                                                                                                                                                                                                                                                                                                                 232 -LAVKEVETLLTSIDE------LAKAIGKKIKNDV------SLDNEADHN 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 VEVLSKAAKE------MLANSVKE------LTSPVVAESPAMVNNSG-- 198
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                                                                                                                                                                                                                                                                             GSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDD 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.2%; Score 169.5; DB 6; Length 1313; 22.2%; Pred. No. 0.0013; valive 60; Mismatches 140; Indels 213;
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GENERAL INFORMATION:
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
                                                APPLICANT:
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NAME/KEY: MISC_PEATURE
LOCATION: (1881)...(1881)
OTHER INFORMATION: X=any amino acid
US-10-032-585-7646
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Best Local Similarity 20.7
Matches 98; Conservative
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
LENGTH. 1881
TYPE: PRT
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Yam...
Roemer, r...
Jiang, Bo
Jone, Charles
Howard
                                                  Trawick, John D. Yamamoto, Robert Roemer, Terry
                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                       Wall, Daniel
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                                                                                                                                                      Robert
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; LOCATION: (1881)..(1881)
; OTHER INFORMATION: X-any amino acid
US-10-072-851-15590
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US-09-708-427-15045
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                                                                                                                                                                                                       Sequence 15045, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                      CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15045
ORGANISM: Arabidopsis thaliana
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                                                      ENGTH: 1304
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Local Similarity 20.7%; Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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                                                                                                                                                                                                                                                             DNA FRAGMENTS
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; ORGANISM: Streptococcus pneumoniae US-09-748-875-14
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-748-875-14
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                                                      TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
LENGTH: 589
                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09748875 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.1
Best Local Similarity 22.3
Matches 115; Conservative
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NAME/KEY: misc_feature
LOCATION: 1..1304
OTHER INFORMATION: Xaa is
NAME/KEY: misc_feature
LOCATION: 1..1304
OTHER INFORMATION: Ceres S
                                                                                                                                                                                                                                                                                                                    APPLICANT: BRILES et al.
                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 ALSHAEEATKIAEIHAEKAEILASELGRLKALLGSKEEKEAIEGNEIVSKLKSEIELLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IELLKKDKAKAIDDLKESEKLVEEANEKLKEALAAQKRAEESFEVEKFR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TNK-----LKEKHT-DLG------KEGVTDADAKEA 142
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Pred. No. 0.0015;
;9; Mismatches 128;
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; ORGANISM: Streptococcus
US-09-748-875-61
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; Sequence 61, Application US/09748875
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
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RIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 61
LENGTH: 690
TYPE: PRT
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR FILE REFERENCE: 454312-3140
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CURRENT FILING DATE: 2000-12-26
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                      QKKVEEAKKKAEDQKEKDRRNYPTITYKTLELEIAESDVEVKKAELELVKVKAKESQDEE 208
                                                                                                                             LDTE-----YNHNGSLLAGAYAIS-----TLIKQKLDGLKNEGLKEKIDA 110
                                                         AKKCSETFTNKLKEKHTD------LGKE-GVTDADAKEAILKTNGTKTKGAEELG 158
                                                                                            LITKLSEIKKKYLYDLKVNVLSEAELTSKTKETKEKLTATFEQFKKDTLPTEPEKKVAEA
                                                                                                                                                                          EGVRSGNNLTVTSSGQDISKKYAD
                                                                                                                                                                                                    ESVK-GPNLT-----EISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIH-ONNG 70
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                                                                                                                                                                                                                                                109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLFES-VEVLSK------AAKEMLANSVKELTSPVVAES------
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25.1%;
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                                                                                                                                                                                                                                         Score 158; DB 5; 1
Pred. No. 0.0035;
9; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.0028;
49; Mismatches 149;
                                                                                                                                                                    ----EVESHLESILKDVKKNLKKVQHTQNVG 88
                                                                                                                                                                                                                                                                            Length 690;
                                                                                                                                                                                                                                           Indels 128;
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; ORGANISM: Streptococcus pneumoniae
US-09-748-875-1
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GENERAL INFORMATION:
APPLICANT: BRILES et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 2000-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/PRIOR FILING DATE: 1999-04-23
                             304 KCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAK 363
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SKKEELTSKTKAELT-----AAFEQFKKDTLKPE----KKVAEAEKKVEEAKKKAKDQK 409
                                                                                                     IDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAK
                                                                                                                                                                                                                                                                                                                                                      LITKLSEIKKKYLYDLKVNVLSEAELTSKTKETKEKLTATFEQFKKDTLPTEPEKKVAEA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESVK-GPNLT-----EISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIH-QNNG
                                                                    ------KKMLSEIQLDRR-KHTQNV-----NL-NIKLSAIKTKYLYELSVLKEN
                                                                                                                                          VSGELATPDKKENDAKSSDSSV--GEETLPSPSLNMANESQTEHR-----KDVDEYI--
                                                                                                                                                                            -----PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTS
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25.1%;
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Pred. No. 0.0035;
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Length 691; Indels 128;

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US-09-748-875-62

Sequence 62, Application US/09748875

GENERAL INFORMATION:

APPLICANT: BRILES et al.

APPLICANT: BRILES et al.

APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR FILE REFERENCE: 454312-3140

CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT APPLICATION NUMBER: 09/298,523

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR FILING DATE: 1999-04-23

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATOLOGICAL SOURCE AND USES THEREFOR PRIOR FILING DATE: 1999-04-23

LENGTH: 701

TYPE: PRT

TYPE: PRT

SECURIOR SECURIOR SOURCE AND USES THEREFOR PRIOR FILING DATE: 2.1
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US-09-748-875-2
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Sequence 2, Application US/09748875
GENERAL INFORMATION:
APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
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                                                                                                                                                                                                                                          E-----MLTNSVKEL
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                                                                   EPITOPIC
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CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,53
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 2
LENGTH: 707
TYPE: PRT
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Best Local Similarity
  410
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E----MLTNSVKEL
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EEDRRNYPTNTYKTL
                                                                              SKKEELTSKTKAELT-----AAFEQFKKDTLKPE----KKVAEAEKKVEEAKKKAKDQK 409
                                                                                                                 KCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAK
                                                                                                                                                                                                                                                                                  -----PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTS 243
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                                                                                                                                                              -----KKMLSEIQLDGR-KHTPNV-----NL-NIKLSAIKTKYLYELSVLKEN 359
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25.1%;
  424
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Pred. No. 0.0036;
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Search completed: March 18, 2002, 09:58:16 Job time: 374 sec

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Title:
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A; Molecule type: DNA A; Residues: 1-210 <jand a;="" combination="" cross-reference="" cross-references:="" embl:x69596;="" in="" nid:g311391;="" of="" pid:g311392="" pidn:caa49306.1;="" t<="" th="" the=""><th>RESULT 1 G70218 Gynater surface protein C - Lyme disease spirochete C;Species Borrella burgdorferi (Lyme disease spirochete) C;Species Borrella burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #sequence Revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #tex</th><th>31 632 34.3 214 2 S69916 Outer surface prot of the surface prot outer surface prot outer</th></jand>	RESULT 1 G70218 Gynater surface protein C - Lyme disease spirochete C;Species Borrella burgdorferi (Lyme disease spirochete) C;Species Borrella burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #sequence Revision 13-Feb-1998 #text_change 21-Jul-2000 C;Date: 13-Feb-1998 #tex	31 632 34.3 214 2 S69916 Outer surface prot of the surface prot outer

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A;Reference number: $72669
A;Accession: $72669
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A:Cross-references: EMBL:X69589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Variety: strain Pr
C; Date: 15-Feb-1997
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Best Local
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MOLECULE type: DNA
// Residues: 1-124 / D'/126-139 / E',141-210 <JAW>
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86; Conservative
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Pred. No. 1.5e-36;
2; Mismatches 1; Indels
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A;Title: Evolution of the Borrelia burgdorferi outer surface prote A;Reference number: I40104; MUID:95286481
A;Accession: I40129
A;Accession: I40129
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-177 <RES>
A;Residues: 1-177 <RES>
                                                                                                    A;Gene: ospC
C;Superfamily:
                                                                                                                          A;Cross_references: EMBL:X84783; NID:g793825; PIDN:CAA59254.1; PID:g793826
                                                                                                                                                                                                                                                                            outer surface protein C - Lyme disease spirochete (strain TXGW) (fragment) C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 02-Aug-196 #sequence_revision 02-Aug-196 #text_change 26-May-200-C:Accession: I40129; S54199
Query Match
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R;Livey, I; Gibbs, C.P.; Schuster, R.; Dorner, F.
MOL. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation in A;Reference number: S70255; MUID:96296448
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Best Local Similarity 99.4
180; Conservative
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A/Title: Expression and sequence of outer surface protein C A/Reference number: 140143; MUID:95154673
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A; Residues: 1-210 <RES>
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C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 12-Aug-196 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I40144; S70282
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                                                                                  Lyme disease spirochete surface protein
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De: strain 297
                           46.3%;
98.9%;
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99.48;
     Score 853; DB Pred. No. 3.6e 0; Mismatches
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Pred. No. 2.8e-34;
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                       DB 2;
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                                  Length 177;
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A;Cross-references: EMBL
A;Experimental source: s
C;Genetics:
A;Gene: ospC
C;Superfamily: Lyme dise
                                                                                                                    outer surface protein C - Lyme disease spirochete C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_(C:Accession: S70279 R:Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 A;Reference number: S70255; MUID:96296448 A;Accession: S70279
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R;Stevenson, B.; Barthold, S.W.
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A;Residues: 1-193 <LIV>
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C; Superfamily:
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A;Molecule type: DNA
A;Residues: 1-211 <RESS
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Itle: Expression and sequence of outer surface protein eference number: 140143; MUID:95154673

VAccession: 140145
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   Lyme disease spirochete surface protein
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                                                EMBL:L42898; NID:g858729;
ce: strain 25015
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Pred. No. 1.
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 outer surface protein C precursor - Bot C; Species: Borrelia afzelii C; Date: 04-Sep-1997 #sequence_revision C; Accession: I40277 R; Fukunaga, M.; Hamase, A. J. Clin. Microbiol. 33, 2415-2420, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-193 <LIV>
A; Cross-references: EMBL: L42895; NID: g858723;
A; Cross-references: Strain 28354
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C;Superfamily: Lyme
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A;Title: Evidence for lateral transfer and recor A;Reference number: S70255; MUID:96296448
A;Accession: S70287
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Pred. No. 1.1
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C:Superfamily: Lyme disease spirochete surface protein
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A;Variety: strain pBre
C;Date: 06-Dec:1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
C;Accession: S69918; S72674; I40103
R;Jauris-Heipke, S:; Liegl, G: Preac-Mursic, V.; Roessler, D.; Schwab, E.; Soutschek, F.;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of Borrelia A; Reference number: I40047; MUID:95395018
A;Accession: S69918
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-152, 'E', 154-211 <ROE>
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A;Residues: 1-211 <JAU>
Noss-references: EMBL:X81522; NID:g872021; PIDN:CAA57242.1; PID:g872022
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A;Accession: 140277
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: nucleic
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Best Local Similarity 75.1
Matches 145; Conservative
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                                                                                                                             1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 AIGOKI-QNNGLAAEADKNGSLLAGAYAISTLIKQKLDGLKGLEGLNKEIAEAKKCSEAF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
     NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS 178
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                                       IGKKIKNDGSLGDEANHNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 135
                                                            IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETET 119
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                                                                                                              ISCNNSGKDGNISANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEL-AKA 75
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75.1%;
                                                                                                                                                                                        ; Score 677.5; DB 2;
; Pred. No. 5.3e-25;
11; Mismatches 30;
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Pred. No. 2.8e-25;
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                                                   Query Match
Best Local
                                Matches
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A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
                                                  A;Cross-references: EMBL:L42871; NID:g858738; PIDN:AAB37014.1; PID:g1695229
A;Experimental source: strain VS461
                                                 C; Genetics:
                                                                                              A; Molecule type: DNA
A; Residues: 1-191 <LIV>
                                                                                                                             A; Status: nucleic acid sequence not
                                                                                                                                               A; Reference number: S70255; MUID: 96296448 A; Accession: S70278
                                                                                                                                                                         R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination
                                                                                                                                                                                                                                          outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_
                                                                                                                                                                                                                                      C; Accession:
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A;Cross-references: GB:D49379; NID:g1041107; PIDN:BAA08377.1; PID:g1041108
C;Superfamily: Lyme disease spirochete surface protein C
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C;Date: 04-Sep-1997
C;Accession: I40273
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A;Tittle: Outer surface protein C gene sequence analysis A;Reference number: 140269; MUID:96025162
A;Accession: I40273
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                120 NKLKEKHTDLGKEGYTDADAKEAILKINGTKTKGAEELGKLFESVEVLSKAAKEMLANSV 179
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Similarity

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Conservative

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Score 674.5; DB 2; Pred. No. 6.5e-25; 8; Mismatches 25;

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Outer surface protein C precursor - Lyme disease spirochete C;Specles: Borrella burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-1 C;Accession: I40268 R;Margolls, N.; Hogan, D.; Cleplak, W. Gene 143, 105-110, 1994 A;Title: Homology between Borrella burgdorferi OspC and members of A;Reference number: I40268; MUID:94259285 A;Accession: I40268 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: I-211 <RES> A;Cross-references: GB:L25413; NID:g495735; PIDN:AAA22956.1; PID:g4*C;Genetics:
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I40268
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C;Genetics:
A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-191 <RES>
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Best Local 9
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75.5%;
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Pred. No. 6.5e-25;
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RESULT 14
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couter Surface protein C - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_C;Accession: $70280
C;Accession: $70280
C;Accession: $70280
                                                             RESULT
S70277
outer surface protein C - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_C;Accession: S70277
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C;Superfamily: Lyme disease spirochete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dox Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and A;Reference number: S70255; MUID:96296448
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C;Superfamily: Lyme
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hes 143; Conservative
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                                                                                                                                ELTSPVVVESP
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Pred. No. 8.1e-25;
Pred. No. 8.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                         Score 672.5; DB 2;
Pred. No. 8.1e-25;
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Lyme di

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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation in Lyme disea A;Reference number: S70255; MOID:96296448
A;Accession: S7027
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-194 <LIV>
A;Residues: 1-194 <LIV>
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A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein C
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Search completed: March 18, 2002, 09:56:46 Job time: 369 sec
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: /SIDS8/gcgdata
3: /SIDS8/gcgdata
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Gapop 10.0 , Gapext 0
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chime	B. burgdor B. burgdor Borrelia 2	Borrelia Borrelia	Borrelia Borrelia	Borrelia 2		1 outer		B burgdorf	0		urgdorf	outer										lia	lia	1 1a	lia	lia	lia

ALIGNMENTS

RESULT AAB62712 Chimeric - Borrelia sp. Chimeric - Borrelia sp. WPI; 2001-050113/06. N-PSDB; AAF29016. 03-APR-2001 (first entry) AAB62712; AAB62712 standard; Protein; 378 (UYNY) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC. 18-JUN-1999; 99US-0140042 28-DEC-2000. WO200078966-A1 Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick Borrelia sp chimeric ospC protein SEQ ID NO: Dattwyler RJ, Seinost G, Dykhuizen D, 19-JUN-2000; 2000WO-US16915. Ŗ Luft BJ, 28 Gomes-Solecki

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Dattwyler RJ,
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Best Local :
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Chimeric -
                        (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                      19-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                     18-JUN-1999;
                                                                                        28-DEC-2000
                                                                                                       W0200078966-A1
                                                                                                                                              Borrelia; ospC; Lyme disease;
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                                                                                                                                                                   Borrelia
                                                                                                                                                                                   03-APR-2001
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Pred. No. 2.9e-121;
0; Mismatches 0; Indels 0;
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     ВJ,
   Gomes-Solecki
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Best Local :
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                                                       Chimeric -
Chimeric -
                                      WO200078966-A1
                                                                                                Borrelia sp
                                                                                                                  03-APR-2001
                                                                                                                                   AAB62710;
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N-PSDB; AAF29042.
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                                                      Borrelia
Borrelia
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                                                                                                                (first entry)
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18-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 43; Page 150-151; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions of OspC polypeptides from strains of Borrelia which caus Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
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                                                                                                                                                             chimeric ospC protein SEQ
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                                                                                                                                                                                                                                               374
                                                                                                                                      vaccine;
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Pred. No. 1.7e-119;
2; Mismatches 2;
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                                                                                                                                                              ID NO:
                                                                                                                                chimeric protein; tick
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Best Local Sim
Matches 370;
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                                        Chimeric -
                                                                                                                                            Borrelia
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                                                                                                                                                                                                                                                                  AAB62728 standard;
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  WO200078966-A1
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DB; AAF29014.
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                                                                                                    ospc;
                                        Borrelia
Borrelia
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                                                                                                                                            chimeric
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                                                                                                    Lyme
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98.1%;
                                                                                                    disease;
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to Lyme disease -
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d to immunize animals and detect immune responses
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Pred. No. 2.6e-104;
0; Mismatches 25;
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Lyme disease are used
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                                                                                                                                     LKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE
                                                                                                                                                                 gkkihqnngld teynhng sllagaya istlikqkldglkneglkekida akkcset ftnk\\
                                                                                                                                                                           GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
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DB; AAF29043.
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Borrelia
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                                                                                                                                                                                                                                                                                                                                                                 160pp; English
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                                                                                                                                                                                                                                                      85.5%;
                                                                                                                                                                                                                                                                                                                                                                                              polypeptides from strains
1 to immunize animals and (
376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     g,
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ES INC.
                                                                                                                                                                                                                                           Score 1589.5; DB 22;
Pred. No. 1.5e-102;
2; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                              s of Borrelia which cause detect immune responses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric -
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                                                                                                                                                                                                                                                                                                                                Compositions of OspC p
                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                         to Lyme disease
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                                                                                                                                                       EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
               gkkihqnngldteynhngsllagayaistlikqkldglkneglkekidaakkcsetftnk
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d to immunize
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                                                                                                                                                                                          22;
                                                                                                                                                                                         Score 1561; DB 22;
Pred. No. 1.3e-100;
2; Mismatches 27;
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Best Local Similarity
Matches 322; Conserv
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi. B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and less vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions of OspC p
Lyme disease are used
to Lyme disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to Lyme disease.
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(BROO-) BROOK
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)B; AAF29033.
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85.6%; Pred. No. 2
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d to immunize
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2.3e-100;
nes 27;
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        121
                                                                                                                                                                                                                    Claim 43; Page 91-92; 160pp; English.
                                                                                                                                                                                                                                        Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                          Dattwyler RJ,
                                                                                                                                                                                                                                                                                                                        (UYNY) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
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)B; AAF29019.
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                                                                                                                                                370 AA;
                                                                                                 Conservative
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                                                                                             Score 1528.5; DB 22; Pred. No. 2.3e-98; 0; Mismatches 31; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
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                                                                                              Indels
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Query Match
Best Local Sim
Matches 326;

Similarity

86.0%;

Conservative

11;

Score 1525.5; D Pred. No. 4e-98; 1; Mismatches

DB 31;

22;

Indels Length

11; 394;

Gaps

4.

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RESULT 1
AAB62730
ID AAB6
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XX AAB6
XX BOII
XX COM
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                                                      The present invention provides compositions comprising ospC protein chimeric ospC proteins from members of the Borrella genus. These members of the Borrella genus. These members of the Borrella genus. These os Borrella burgdorferi, B. afzelii or B. garinii. These can be used vaccines against Borrelia infection, which is spread by ticks and
Sequence
                                                                                                                                                                                           Claim 43; Page 128-129; 160pp; English
                                                 vaccines against Borrelia infection, to Lyme disease.
                                                                                                                                                                                                                                                  Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                   Dattwyler RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999;
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Chimeric - Borrelia
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DB; AAF29034.
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BROOK BIOTECHNOLOGIES IN
394 AA;
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                                                                                                          These may be
                                                           leads
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84 62

179

143

Matches

Conservative

32;

Mismatches

33;

Indels

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Gaps

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82.0%;

Pred.

No. 4e-96;

Best Local Similarity

299 315

255 239 203

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RESULT 1
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                                                                        Compositions of OspC |
Lyme disease are used
to Lyme disease -
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                                                                                                                             Dattwyler RJ,
                                                                                                                                           (BROO-)
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)B; AAF29030.
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Borrelia
                                                                                                                                                                                                                                                                   chimeric ospC
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                                                                                                                             ВJ,
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                                                                                       of.
                                                                                                                                                                                                                                                    protein;
                                                                                       Borrelia which
                                                                                                                             Gomes-Solecki
                                                                                immune responses
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Query Match

80

. 5%;

Score 1496.5;

DΒ

22;

Length

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. gazinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea

leads and be 6

Lyme

disease.

Sequence

384

Ş.

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea

as leads

and

Claim 43;

Page 117-118; 160pp;

English.

cause

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RESULT 1
AAB62737
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Lyme disease are used
to Lyme disease -
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(BROO-)
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Chimeric -
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                                                                                                                                                                    WO200078966-A1
                                                                                                                                                                                                     Borrelia; ospC; Lyme disease; vaccine;
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                                Claim
                                                                       N-PSDB;
                                                                                          Dattwyler RJ,
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DB; AAF29041.
                                43; Page 147-148;
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                                                                                                        BROOK
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                                                                                                                                                                                                                                                          standard;
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                                                                                                        ES FOUND.
                                English.
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                                                                                                                                                                                                                  SEQ
                                                    from strains of Borrelia which cause animals and detect immune responses
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                                                                                                                                                                                                     chimeric protein;
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                                                                                            ВJ,
                                                                                           Gomes-Solecki
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Lyme

disease.

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AAB62718
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Best Local S
Matches 308
       Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                                                            (UYNY )
(BROO-)
                                      WPI; 2001-050113/06.
N-PSDB; AAF29022.
                                                                                                                                                                Chimeric - Chimeric -
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                                                             Dattwyler RJ,
                                                                                                                                  28-DEC-2000
                                                                                                                                                  WO200078966-A1
                                                                                                                                                                                       Borrelia; ospC; Lyme disease; vaccine;
                                                                                                                                                                                                     Borrelia sp chimeric ospC protein SEQ ID NO: 40
                                                                                                                                                                                                                                                    AAB62718 standard;
                                                                                                    18-JUN-1999;
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mes 308; Conser
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                                                                                                                                                                                                                                                                                                  SKAAKEMLTNSVKELTS 378
                                                                                                                                                                                                                                                                                           skaaqaaltnsvkeltn 398
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                                                                            UNIV NEW YORK STATE RES FOUND. BROOK BIOTECHNOLOGIES INC.
                                                                                                                                                                Borrelia
Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                   2000WO-US16915.
                                                                                                                                                                                                                     (first entry)
                                                              Seinost
                                                                                                    99US-0140042
                                                                                                                                                                                                                                                    Protein; 368
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                                                             Dykhuizen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1493.5; D
Pred. No. 7e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
             from strains of Borrelia which cause animals and detect immune responses
                                                                                                                                                                                       chimeric
                                                             Luft
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                                                             BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                             Gomes-Solecki M;
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Chimeric - Borrelia
WPI; 2001-050113/06
                    Dattwyler RJ,
                                                                                            19-JUN-2000;
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                                                                         18-JUN-1999;
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Q49577	044883	P94233	Q9z6c7	P94231	031114	Q9rqr8	044727	P94244	P94247	050619	P96572	Q44705	050624	80596d	P94242	044976	P96573	P94245	Q44726	P96571	Q44671	Q9kim5	Q44977	031122	Q49576
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INE-96296448; PubMed-8709845; y I., Glbbs C.P., Schuster R., Dorner F.; bence for lateral transfer and recombination disease Borrelia.", Microbiol. 18:257-269(1995). ; L42887; AAB36995.1; -rero; IPR001800; Lipoprotein_6. ; PF01441; Lipoprotein_6; 1. m; PD001149; Lipoprotein_6; 1. FER 192 192 ENCE 192 AA; 20287 MW; 11846F7AC84C7E3D	-2000 (TrEMBLrel. 13, Created) -2000 (TrEMBLrel. 13, Last sequence -2001 (TrEMBLrel. 17, Last annotatio SURFACE PROTEIN C (FRAGMENT). Is burgdorferi (Lyme disease spiroch la; Spirochaetales; Spirochaetaceae; axID-139;	S3P3 PRELIMINARY; PRT; 192 A 939B3; 1-MAY-2000 (TrEMBLrel. 13, Created) 1-MAY-2000 (TrEMBLrel. 13, Last sequence 1-JUN-2001 (TrEMBLrel. 17, Last annotatio 9TER SURFACE PROTEIN C (FRAGMENT). 9PC. 19PC. 19P
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_TaxID=139; IN=ID=3626448; PubMed=8709845; INE=96296448; PubMed=8709845; INE=96296448; PubMed=8709845; INE=96296448; PubMed=8709845; INE=96296448; PubMed=8709845; Ince for lateral transfer and recombination disease Borrelia."; disease Borrelia."; disease Borrelia."; Microbiol. 18:257-269(1995).; L42887; AAB36995.1; FPTO; IPR001800; Lipoprotein_6. ; PF01441; Lipoprotein_6; 1. TER 1 1 1 FER 1 192 1 192 1 192 INCE 192 AA; 20287 MW; 11846F7AC84C7E3D	; 2000 (TrEMBLrel. 13, -2000 (TrEMBLrel. 17, -2001 (TrEMBLrel. 17, SURFACE PROTEIN C (FRA	933P3 PRELIMINARY; 933P3, PRELIMINARY; 953P3, PRELIMINARY; 1-MAY-2000 (TrEMBLrel. 13, 1-JUN-2001 (TrEMBLrel. 17, 1-JUN-2001 (TrEMBLrel. 17, 1-JUN-2001 (TREMBLREL 17, 1-JUN-20
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01-FEB-1997
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                               Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
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0UTER SURFACE PROTEIN (FRAGMENT).
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Marti-Ras N., Postic D., Foretz M.,
Submitted (MAR-1997) to the EMBL/Ge
EMBL; U91798; AABB1895.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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MEDLINE-97478003; PubMed-9336916;
Mas N.M., Postic D., Foretz M., Baranton G.;
"Borrelia burgdorferi sensu stricto, a bacterial species 'made
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00TER SURFACE PROTEIN C (FRAGMENT).
BOTTELIA burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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Best Local
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Q9RR53;
Q1-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                  Wang I.N., Dykhuizen D.E., Qiu W., Dunn J.J., Bosler E.M., Lu Genetic diversity of ospC in a local population of Borrelia burgdorferi sensu stricto.";
Genetics 151:15-30(1999).
BMBL: AF02986; AAB86543.1;
InterPro: IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
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Bacteria; Spirochaetales; Spirochaetaceae; Borr
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STRAIN=2-1498 CA4;

Probert W.S., Crawford M.R., Cadiz R.B., LeFebvre R.B.,

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL, L81131; AAB06569.1; -...

InterPro; IPR001800; Lipoprotein_6.

Pfam, PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
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IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                           ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
                                                                 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDETAAKA
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                                                                                                                                                                                                                                              193
193 AA;
                                                                                                                                     Conservative
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98.9%;
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                                                                                                                                                          Score 908; DB 2;
Pred. No. 1.3e-34;
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Pred. No. 1.1e-34;
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Best Local S
Matches 181
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"Population dynamics of a naturally of
Borrella burgdorferi clones";
Infect. Immun. 67:3709-5716(1999).
EMBL; AR074464; AAD23911.1;
InterPro; IPR001800; Lipoprotein_6.
Pfom; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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O9R7B2 PRELIMINARY; PRT; 182 AA. 09R7B2; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 01TER SURFACE PROTEIN C (FRAGMENT). Borrelia burgdorferi (Lyme disease spirochete). Bacteria; Spirochaetales; Spirochaetaceae; Borrel
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Bacteria; Spirochaetales;
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SEQUENCE 182 AA;
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                                                                                                                                                             Wang I.-N., Dykhuizen D.E., Dunn J.J., Luft B. Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF029869; AAB86552.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marti-Ras N., Postic D., Foretz M., Submitted (MAR-1997) to the EMBL/Ge EMBL, U91797; ANBB1894.1; ... InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TremBLrel.
01-JAN-1998 (TremBLrel.
01-JUN-2001 (TremBLrel.
OUTER SURFACE PROTEIN C
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Borrelia burgdorferi sensu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97478003; PubMed=9336916;
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Lipoprotein_6; 1.
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                                                                                                       MW;
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Q44719;
01-NOV-1996
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NON_TER
NON_TER
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EMBL; L42893; AAB37001.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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Bacteria: Spirochaetales; Spirochaetaceae; Borr
                                                                     375
                                                                                   122
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                                                                                                                                                                                                                                                                                                   MEDLINE=96296448; PubMed=8709845;
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STRAIN=297;
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192 A
(TrEMBLrel.
               PRELIMINARY;
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; 20472 MW;
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99.48;
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K MEDLING=95:54673; pubMed=7851744;

Stevenson B., Barthold S.W.;

R Expression and sequence of outer surface protein C among Parents in Sequence of Sequence of Sequence Protein Sequence of Sequence Protein Sequence of Sequence Protein Sequence Sequence 10 AA; 22526 MW; 20672991D584E4EE: CRC64;
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Best Local
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Q44999;
01-NOV-1996;
01-NOV-1996;
01-JUN-2001;
            NON_TER
                                         "Evolution of the Borrelia burgdorferi
J. Bacteriol. 177:3036-3044(1995).
EMBL; X84783; CAA59254.1;
Interpro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                     Theisen M., Borre M., Mathiesen M.J.,
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                                                                                                                                                                                                  01-NOV-1996 (TIEMBLIE1. 01, Created)
01-NOV-1996 (TIEMBLIE1. 01, Last sequence update)
01-JUN-2001 (TIEMBLIE1. 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
                                ProDom; PD001149;
                                                                                                 Hansen K.;
                                                                                                                               STRAIN-TXGW;
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                                                                                                                   MEDLINE~95286481;
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Bacteria; Spirochaetales; s
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Spirochaetales; s
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                              Lipoprotein_6; 1.
49; Lipoprotein_6;
  AA;
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Last
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Pred. No. 3.1e-33;
0; Mismatches 1
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annotation
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Query Match

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Best Local Similarity 98.
Matches 175; Conservative
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O9REH7;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                       O9R7B4 PRELIMINARY: PRT; 175 AA.
09R7B4; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update
01-JUN-2001 (TrEMBLrel. 17, Last annotation update
OUTER SURFACE PROTEIN C. (FRACKENT).
Borrelia burgdorferi (Lyme disease spirochete).
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"Polymorphism in ospC gene of Borrelia burgdorferi
immunoreactivity of OspC protein: implications for
use of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
EMBL; X73622; CAA52001.1;
InterPro; IPR001800; Lipoprotein_6.
pfam; PF01441; Lipoprotein_6; 1.
ProDom: PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-B31;
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00TER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
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                                                                                                                        InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                             Marti-Ras N., Postic D., For Submitted (MAR-1997) to the EMBL; U91801; AAB81898.1; -
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Ras N.M., Postic D., Foretz M., Baranton
"Borrelia burgdorferi sensu stricto, a bi
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0UTER SURFACE PROTEIN C (FRAGMENT).
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                                     Bacteria;
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STRAIN-TETS;
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RESULT 1
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SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
                                                                                                                                                                                            MEDLINE-96025162; PubMed-7494039;
Fukunaga M., Hamase A.;
"Outer surface protein C gene sequence analysis
burgdorferi sensu lato isolates from Japan.";
J. Clin. Microbiol. 33:2415-2420(1995).
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STRAIN-ATCC 35210 / B31;

STRAIN-94041630; PubMed-8225587;

MEDLINE-94041630; PubMed-8225587;

Padula S.J., Sampieri A., Dias F., Szczepanski A., Ryan R.W.;

"Molecular characterization and expression of p23 (OspC) from American strain of Borrelia burgdorferi.";

Infect. Immun. 61:5097-5105(1993).
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Plasmid 1p54.
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                              STRAIN-PKO;
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Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Signal; Plasmid; Antigen;
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-i- FUNCTION: ATTACHED TO THE OUTER MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                             50.4%;
                                    PARTIAL
                                                                s disease spiroch
Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
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                                                                                                                                                                                                                                                                                                                                                                          Score 928; DB 1;
Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
OUTER SURFACE PROTEIN C.
N-ACYL DIGLYCERIDE (BY SIMILARITY).
7A4FC978F91777BF CRC64;
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease spirochaete,
   F.
                                  SEQUENCE
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                                                                           spirochete)
   Preac-Mursic
                                                                                                                                                   212
                                                                                                        update)
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                                                                Borrelia
   ۷.,
                                                                                                                                                                                                                                                                                                                                                                                     Length 210;
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RESULT 3
VM24_BORHE
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VM24_BORHE
VM24_BORHE

F32778;

f 01-OCT-1993 (Rel. 27, Created)
T 01-OCT-1993 (Rel. 27, Last sequence updated)
T 01-FEB-1994 (Rel. 28, Last annotation up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 135
                                                          Borrelia
Plasmid.
SEQUENCE
                            NCBI_TaxID=140;
                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; Lipoprotein; Signal; Plasmid; Antigen SIGNAL 1 18 BY SIMILARITY CHAIN 19 212 OUTER SURFACE PROTEIN C. LIPID 19 19 N-ACYL DIGLYCERIDE (BY S. SEQUENCE 212 AA; 22499 MW; C206C231FBFZE7D4 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               119
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J. Clin. Microbiol. 31:2570-2576(1993).

-i. FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.

-i. SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-205
STRAIN-DK26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soutschek E.; "Molecular analysis and expression of a Borrelia burgdorfer1 gene encoding a 22 kDa protein (pC) in Escherichia coli."; Mol. Microbiol. 6:503-509(1992).
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135; Conserv
                                        Spirochaetales;
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                                      Spirochaetaceae;
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Pred. No. 1.4e
14; Mismatches
                                                                                                    LIPOPROTEIN
                                                                                                                                   update)
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                                                                                                   24 PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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Best Local
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InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIPID
SEQUENCE
                                                                                                                                                       002448:
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 3 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
Restrepo B.I., Kitten T., Carter '
"Subtelomeric expression regions
                                            STRAIN-SSP. HS1 SI
                                                                                                                                                                                                                                              BORHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are highly polymorphic.";
Mol. Microbiol. 6:3299-3311(1992).
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MEDLINE-93133110; PubMed-1484486;
                                                                                                     Bacteria;
                                                                                                                   Plasmid
                                                                                                                              Borrelia hermsii
                                                                                                                                               VMP3
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                                                                                  NCBI_TaxID=140;
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                                                                                                  Spirochaetales;
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214 /
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                                                                                                  Spirochaetaceae;
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N-ACYL DIGLYCERIDE
; F1583F510246F7C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 404.5;
Pred. No. 3.
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VARIABLE MAJOR OUTER MEMBRANE
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 C.J., Infante D., Barbour A.G. of Borrelia hermsii linear pla
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nes 59;
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Best Local S
Matches 94
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SEQUENCE
Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;

"Complete nucleotide sequence and deduced polypeptide sequence nonmuscle myosin heavy chain gene from Acanthamoeba: evidence o hinge in the roditke tail.";

J. Cell Biol. 105:913-925(1987).

-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS A ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

-i- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEM INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Signal; Plasmid.
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Mol. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=87308395;
                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1988 (Rel. 09, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat MYOSIN II HEAVY CHAIN, NON MUSCLE. Acanthamoeba castellanii (Amoeba).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P05659;
01-NOV-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKAIGKKI-HQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLK-----NEGLKEKIDA 110
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40,
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215
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N-ACYL DIGLYCERIDE
684C74D35F87C771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 400; DB 1
Pred. No. 5e-12;
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VARIABLE MAJOR OUTER MEMBRANE
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PROSSITE; PS50096; IQ; 1.

Myosin; Colled coil; Actin-binding; ATP-binding; Calmodulin-binding; Myosin; Colled coil; Phosphorylation; Multigene family.

Methylation; Alkylation; Phosphorylation; Multigene family.

MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
PF1NTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                          994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A27224; A27224.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00624; CAA68663.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                    78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head
                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEFILLS, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NOHELICAL TAILPIECE WHERE THE REGULATORY PHOSEHORYLATION SITES RESIDE.

MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSEHORYLATION ON ENZYMATIC ACTIVITY.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 2 IQ DOMAINS.
VDSLKSKLSAAEKSL--KTAKDQNRDLDEQLEDERTVRANVDKQKKALEAKLTELEDQVT
                                                                                 TDA--DAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE-------
                                                                                                                                                                     ELQEETSASNDILEQKRKLEAEKGELKASLEEEERNRKALQEAKTKVESERNELQDKYED
                                                       RNELDDVTATKLQLEKTKKSLEEELAQTRAQLEE-EKSGKEAASSKAKQLGQQLEDARSE
                                  ---LTSPVVAESPAMVNNSGKDGN-----
                                                                                                                                        NGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDA----AKKCSETFTNKLKEKHTDLGKEGV
                                                                                                                                                                                              EISKKITDSNAVLLAVKEVEA----LLSSIDE-----IAAKAIGKKIHQNNGLDTEYNH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
                                                                                                                                                                                                                                                  Similarity
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848
848
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                                                                                                                                                                                                                             Score 176.5; DE 
Pred. No. 0.41; 
68; Mismatches 1
                                                                                                                                                                                                                                                                                                                       METHYLATION (TRI-) (POTENTIAL)
ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                          NONHELICAL TAILPIECE.
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                                                                                                                                                                                                                                                                                                2CE49BE51173D17E CRC64;
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                            TSANSADESVKG - - PNLTEISKKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                               137;
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01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92315338; PubMed=1617731; Galinski M.R., Medina C.C., Ingra
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Q00799;
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01-APR-1993 (Rel. 25, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
RETICULOCYTE BINDING PROTEIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galinski M.R., Medina C.C., Ingravallo P., Barnwell J. "A reticulocyte-binding protein complex of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1261 LERLEEELLTAQEARAAAEK-NLDKAN--LELEELRQEADDAARDNDKLVKDNRK 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1161 ALDGQKNA----AAAQAKTLKTQVDETKRRLEEAEASAARLEKERKN--ALDEVAQ-----
                                                                                                                                                                                                              22 KGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA--IGKKIHQNNGLDTEYNHNG
                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226
                                KTLEGEVNA-----LKASSDNHEHVQSKSEPV-NPALSEIEKEET------DIDS
                                                                                                                                                             SLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL---KEKHTDLGKEGVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. HUMAN RETICULOCYTE CELLS.
                                                         KELTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVET
                                                                                      KSYDNIIALEKQTELQNLRNSFTQEKTNTNSDSKLEKIKTDFES-
                                                                                                                                     -----YLKVVLINQ------YKNKISSIKSKEEAVSVKIGNVSKKHSELSKITÇSD
                                                                                                                                                                                      KNTNELDVHKNIQDAYKVALEI-----LAHSDEIDTKQKDSSKLIEMGNQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69:1213-1226(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ESNAVVLAVKEVETLLTSIDEL------AKAIGKKIKNDVSLDNEADHNGSL
                                                                                                                                                                                                                                                93;
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                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 Receptor; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement
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1251 AA;
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                        Score 170;
Pred. No. 0
-AIGKKIKNDVSLDNEADHNGSLISGAYL-----
                                                                                                           -KTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSV
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its content
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Best Local S
Matches 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last amotation update)
HYPOTHETICAL 222.8 KDA PROTEIN C1F3.06C IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPACIF3.06C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4896
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 KISAIKDSGELKAEIEKAKKCS----EEFTAKLKGEHTDLGKE----
                                                                                                                                                                                                                                                                                    DKMVKQVSSQLEEARSSLAHATGKLAEINSERDFQNKKIKDFEKIEQDLRACLNSSSNEL
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                                                               VKEVETLLTSIDELAKAIGKKIKNDVSLDNE------ADHNGSLISGAYLISNLITK
                                                                                                                        LANSVKELTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESN-AVVLA
                                                                                                                                                          LKGELQTEISNSEHLSSQLSTLAAEKEAAVATN--
                                                                                                                                                                                                                      KEKSALIDKKDQELNN--LREQIKEQKKVSESTQSSLQSLQRDILNEKKKHEVYESQLNE
                                                                                                                                                                                                                                                     ---STLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL--
                                                                                                                                                                                                                                                                                                               -----TEYNHNGSLLAGAYAI
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                              LKDTSSKLOQL-QLERANFEQKESTLSDENNDLRTKLLKLEESNKSLIKKQEDVDSL-EK
                                                                                          LAKSVMQL-----KENEQNFSSLDTSFK--KLNESHQELENNHQTITKQ
                                                                                                                                                                                                                                                                                                                                                                                                              107;
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1957 AA;
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23.1%;
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Pred. No. 1
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01-AUG-1988
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLIND-#86111835; PubMed-3511046;
Hollingshead S.K., Fischetti V.F., Scott J.R.;
Hollingshead S.K., Fischetti V.F., Scott J.R.;

"Complete nucleotide sequence of type 6 M protein of the Streptococcus. Repetitive structure and membrane anchor."

J. Biol. Chem. 261:1677-1686(1986).
DOMAIN
                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                         DOMAIN
                                                                                                                              CHAIN
                                                                                                                                                                                                                                 InterPro; IPR001899;
InterPro; IPR003345;
                                                                                                                                                                                                                                                          EMBL; M11338; AAA26920.1; PIR; A26297; A26297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott J.R., Pulliam W.M., Hollingshead S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 43-122 FROM N.A. MEDLINE=85166224; PubMed=3885219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes
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                                                                                       DOMAIN
                                                                                                    TRANSMEM
                                                                                                                DOMAIN
                                                                                                                                          SIGNAL
                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                       Pfam; PF00746; Gram_pos_anchor; Pfam; PF02370; M; 9.
                                                 DOMAIN
                                                               DOMAIN
                                                                            DOMAIN
                                                                                                                                                                   Virulence; Phagocytosis;
                                                                                                                                                                               PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        750 L--SSELTKSSEDVKRLTANVETLTQDSKAMKQSFTSLVNSYQS
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                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE SIMILARITY: TO OTHER M PROTEINS. SIMILARITY: TO OTHER STREPTOCOCCAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT
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                                                                                                                                                                                             PR00015; GPOSANCHOR.
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8 (Rel. 08, Last sequence up
1 (Rel. 40, Last annotation
SEROTYPE 6 PRECURSOR.
                                                458
478
478
157
279
                                                                                                                                                       Coiled
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457
477
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138
269
347
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                                                                                                                                                                                                                                              Gram_pos_anchor
                                                                                                                                                       coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Clostridium group;
                                                                                                                                                                   Cell wall;
                                                                                                                                                    Signal
                                 1.0 X / AA INCL...
4.5 X 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMINO ACIDS.
GLY/PRO-RICH
CONSERVED IN
                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                               M PROTEIN, SEROTYPE 6.
EXTRACELLULAR (POTENTIAL).
                         HYDROPHILIC
                                                                                                    MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                           7 AA TANDEM REPEATS
                                                                                                                                                                  Duplication;
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(CELL WALL-SPANNING).
GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                   Repeat;
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                                                                                                                                                                     Antigen;
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RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                M12_STRPY STANDAND,
P19401;
O1-NOV-1990 (Rel. 16, Created)
O1-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 SEROTYPE 12 PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CS24 / Serotype M12;
MEDLINE-88058777; PubMed-2445730;
Robbins J.C., Spanier J.G., Jones S.J., Simpson W.J., Clea
"Streptococcus pyogenes type 12 M protein gene regulation
                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes
                                                                                                                                                                                                                                                                                           NCBI_TaxID=1314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                  Bacteriol. 169:5633-5640(1987).

- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE P
SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND
IN THE REGION OF THE MEMBRANE ANCHOR.
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                                                                                                                                              PHAGOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTEKEKAELQAKLEAEAKALKEQLAKQAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLKKTLDETVKDKIAKEQESKETIGTLKKILDETVK----DKIARE-QKSKQDIGALKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDQNKNLTTE---NKELKAEENRLTT-----ENKGLTKKLSEAE---EEAANKERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKELTSPVVAESPAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKEAIGTLKKTLDETVKDKIAKEQESK----ETIGTLKKTLDETVKDKIAKEQESKETIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNDKLTTENNNLTDQN----KNLTTENKNLTDQNKNLTTENK-------NL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAKKDEGNKVSEASRKGLRRDLDASREA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHTDLGK-EGVTDADAKEAILKTNGTKTKGAEELGKLFESVE--VLSKAAKEM----LAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SKAAKEMLTNSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%;
                                                                                                                                                                                                                                                                                                                  Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 167; DB 1;
Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS.
68F87F28DB53A448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373
                                                                                                                                                                                                              Simpson W.J., Cleary P.P.; in gene regulation by upstr
                                                                                                                             PROTEIN. CELL WALL.
                                                                                                    STAPHYLOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                                               group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KKQVEKDLANLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 88
                                                                                                                                                                                                                upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357
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   OC CO CO DT DT DAC
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USO1_YE
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Olyman Olyman (National Stanton)

USO1, VEAST STANTON

P25386;
T 01-MAY-1992 (Rel. 22, Created)
T 01-MAY-1992 (Rel. 22, Last sequence update)

OT 20-AUG-2001 (Rel. 40, Last annotation update)

TAMPRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                          INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
USO1 OR INT1 OR YDLO58W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
NCBI_TaxID=4932
             Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virulence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001899; Gram_pos_anchor
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A60115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M18269; AAA88573.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 DLL----RHKQEIAEKENVIS-----KLNG-ELQPLKQKVD-----ETDRNLQQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GNTSANSADESVKGPNLTEISKKITDSNAVLLAV-KEVEALLSSIDEIAAKAIGKKIHQN 68
| ::|| | :||: | | :||:| | | |:::|
| SKIGIDNADLKAK---TTELEKSVEEKNDVLSQIKKELEEAEKDIQ-----FGREVHAA 165
                                                                                                                                                                                                                                      QLAKQAEEL
                                                                                                                                                                                                                                                                    MLTNSVKEL
                                                                                                                                                                                                                                                                                                                     LGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNL----
                                                                                                                                                                                                                                                                                                                                                                                                                     AELAKVTEQKQILDASRKGTARDLEAVRKSKKQQVEAALKQLEEQNKISEASRKGLRRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V----AESPAMVNNSGKDG-----NTSANSADESVKGP-----
                                                                                                                                                                                                                                                                                              LDASREAKKQVEKA-LEEANSKLAALEKLNKDLEESKKLTEKEKAELQAKLEAEAKALKE
                                                                                                                                                                                                                                                                                                                                                                                       SLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --KQKVLSLEQQLAVTKENAKKDFELAALGHQLADKEYNAKIAELESKLADAKKDFELAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EISKKITESNAVVLAVK------EVETLLTSIDE---LAKAIGKKIKNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGHQHAHNEYQAKLAEKDGQIKQLEEQKQILDASRKGTARDLEAVRQAKKATEAELNNLK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAA - - KEMLANSVKELTSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF02370; M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00746; Gram_pos_anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 22.0
97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phagocytosis; Ce
ane; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551
44
505
542
                                                                                                                                                                                                                                                                    373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRAM_POS_ANCHORING; 1.
ytosis; Cell wall; Duplication; Repeat; Antigen; biled coil; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                >564
550
>564
505
541
547
           Saccharomycetaceae;
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62904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 167; DB
Pred. No. 0.36
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLY/PRO-RICH
CONSERVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEMBRANE ANCHOR COILED COIL (PO'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M PROTEIN, SE
                                                                                                                                                                                                                                                                                                                                                           -KKQVEKDLANLTAELDKVKEEKQISDASRQGLRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5F1549DACAA77B46 CRC64;
             Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN GRAM-POSITIVE COCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEROTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                            SKAAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -NLT
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                                                                                                                                                                                                                                                                                              483
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                                                                                                                                                                                                                                                                                                                                                           424
                                                                                                                                                                                                                                                                                                                                                                                       319
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                                                                                                                                                Query Match
Best Local Similarity
Matches 102; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X54378; CAA38253.1; -.
EMBL; L03188; AAB00143.1; -.
EMBL; U53668; AAB66659.1; -.
PIR; A38455; A38455.
HSSp; P80220; IDIP.
SGD; S0002216; US01.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                        DOMAIN
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SEQUENCE FROM
STRAIN-X2180-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A cytoskeleton-related gene, usol, protein transport in Saccharomyces of Cell Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bai Y., Symington L.S.;
Submitted (MAY-1996) to
-1- FUNCTION: REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioliformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-1993) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hostetter M.K., Herman D.J.,
Kendrick K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91185402; PubMed-2010462;
 985
                                                                          929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE OF 1-8 FROM N.A.
                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF A COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: CYTOPLASMIC. MEMBRANES. PROBABLY PRESENT ON VES
                                                                                                               CNNSGKDG-----
VEESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIEKNIEQLKKTISDLEQTKEEIISK
                                     IDEIAAKAIGKKIHQNNGLD--TEYNHNGSLLAGAY---
                                                                        CNNLSKEKEHISKELVEYKSRFQSHDNLV--AKLTEKLKSLANNYKDMQA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H., Hirata
                                                                                                                                                                                                                                                               465
991
1172
847
924
1253
1319
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1581
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                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                             724
1790
487
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1786
8487
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1319
1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transport;
                                                                                                         ----NTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSS
                                                                                                                                                                 8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the
                                                                                                                                                                                                                                             206424
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                                                                                                                                                                                                                                GLOBULAR HEAD.

COLLED COLL (POTENTIAL).
COARGED (HYPER-HYDROPHILIC).
CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN FU
ASP/GLU-RICH (ACIDIC).
G -> E (IN REF. 2).
E -> K (IN REF. 2).
I -> V (IN REF. 2).
I -> V (IN REF. 2).
N -> S (IN REF. 2).
G -> S (IN REF. 2).
I -> V (IN REF. 2).
I -> V (IN REF. 2).
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73; Mismatches
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P49454; Q13274; Q13171;
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20-AUG-2001 (Rel. 40, Last annot
CENP-F KINETOCHORE PROTEIN (CENT
                                                                                                               J. Biol.
[5]
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MEDLINE-95348175; PubMed-7542657;

Liao H., Winkfein R.J., Mack G., Rattner J.B., 1

"CENP-F is a protein of the nuclear matrix that kinetochores at late G2 and is rapidly degraded J. Cell Biol. 130:507-518(1995).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 2194-3210 FROM N.A. MEDILINE-9533646; PubMede-7612011; MEDILINE-9533646; PubMede-7612011; Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Li Q., Medsger T.A. Jr., Medical Policy No. 100 Med
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CHARACTERIZATION.
MEDLINE-98437347; PubMed-9763420;
Chan G.K.T., Schaar B.T., Yen T.J
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Mammalia; Eutheria;
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                                                                                                                                                 centromere/kinetochore targeting, and J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                                                                                                                                   CHARACTERIZATION. MEDLINE=95370296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that is specifically involved in mitotic-phase Mol. Cell. Biol. 15:5017-5029(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95379848; PubMed=7651420; Zhu X., Mancini M.A., Chang K.-H.,
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J. Cell Biol. 143:49-63(1998).

-i-FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION,
CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH
RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 KEVEALLSSIDEIAAKAIG---KKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLK 100
      IGKKIKNDVSLDNEADHNGSLISGAYLISNL---
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SUBGUNIT: HOMO- OR HETERODIMER.

SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS),

REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF
THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.

DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE.
                                                                                                           PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDELAKA
                                                                                                                                                                     KQIQEKQGQLSELDKLLSSFKSLLEEKEQAEIQIKEESKTAVEMLQNQLKELNEAV----
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   MEDLINE-97452580;
                                                                                          "X-ray structure of the magnesium(II). Dictyostellum discoideum myosin motor Biochemistry 35:5404-5417(1996).
                                                                                                                                                                                                                                                                                                                                                               Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate complex of the truncated head of Dictyostelium discoideum myosin to 2.7-A
                                                                                                                                                                                                       MEDLINE=96206189; Pu
Smith C.A., Rayment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "X-ray structures of the myosin motor discoideum complexed with MgADP.BeFx Biochemistry 34:8960-8972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE=95345067; PubMed=7619796;
                            K-RAY CRYSTALLOGRAPHY (2.1
                                                                                                                                                                                                                                                                                                                                             Biochemistry 34:8973-8981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium myosin heavy chain."; FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (1
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MEDLINE-95345066; PubMed-7619795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagle G., Noegel A., Scheel J., Gerisch G. "Phosphorylation of threonine residues on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Replacement of threonine residues by serine and alanine in a phosphorylatable heavy chain fragment of Dictyostelium myosin FEBS Lett. 269:239-243(1990).
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Lueck-Vielmeter D., Schleicher M.,
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Warrick H.M., de
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Eukaryota: Mycetozoa; Dictyosteliida;
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Conserved protein domains in a myosin heavy
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and MgADP.AlF4-.";
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PIR: A26555; A26556

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PIR: S00250; S00250.

PDB: 1MMD; 17-AUG-96.

PDB: 1MMD; 17-AUG-96.

PDB: 1MND; 17-AUG-96.

PDB: 1MND; 17-AUG-96.

PDB: 1VOM; 23-DEC-96.

PDB: 1LVK; 28-JAN-98.

PDB: 1LVK; 28-JAN-98.

PDB: 1LVK; 28-JAN-98.

D1CtyDb; DD01008; mhcA.

InterPro; IPR000048; IQ.

InterPro; IPR00109; myosin_head.
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Pfam; PF00063; myosin_head; 1.
Pfam; PF000193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; TQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; TQ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Mg.2'(3')-O-(N-methylanthraniloyl) nucleotides bound to the Dictyostelium discoldeum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).
-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.
-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKAI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
   NP_BIND
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MOD_RES
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"X-ray structures of the MgADP, MgATPgammaS, and MgA
of the Dictyostelium discoideum myosin motor domain.
Biochemistry 36:11619-11628(1997).
                                                                                                                                        Myosin; Coiled
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SUBFRAGMENT (SI).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COOLLS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COOLLS.

PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIVATED APPASE ACTIVITY.

MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1
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SIMILARITY: CONTAINS 1 10 DOMAIN.
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DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT II

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM).
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                                    "Sequencing of laminin B chain coiled-coil alpha-helix.";
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MEDLINE=87147212; PubMed=3493487;
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Mammalia; Eutheria;
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                                                                                                            the cDNA encoding the laminin B1 chain r protein containing cysteine-rich repeats. Acad. Sci. U.S.A. 84:935-939(1987).
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MGD; MGI:96743; Lamb1-1.

InterPro; IPR001886; LamNI; Lamhin_EGF-like.

InterPro; IPR001886; LamNI; Lamhin_EGF: InterPro; IPR002049; Lamhinin_EGF: InterPro; IPR002049; Lamhinin_EGF: InterPro; IPR002049; Lamhinin_Legr: InterPro; IPR00053; Laminin_Legr: InterPro; InterPro; Laminin_Legr: InterPro; 
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Laminin EGF-like domain; Cell ad
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EMBL; X05212; CAA28839.1;
PIR; A26413; MMMSB1.
HSSP; P03069; 1ZIM.
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"Cloning of the mouse laminin alpha 4 cDNA. Expression endothelium.";
Eur. J. Blochem. 246:727-735(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. J. BIOChém. 246:727-735(1997).

FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ THE THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH CYHER EXYRACELLULAR MATRIX COMPONENTS.

SUBUNIT: LAMININ IS A COMPLEX GILYCOPROTEITS, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ.

2 (MEROSIN), AND LAMININ-6 (K-LAMININ).

SUBCELLULAR LOCATION: EXTRACELLULAR.

TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPONENT).
SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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LAMININ N-TERMINAL (DOMAIN VI)
4.5 X LAMININ EGF-LIKE REPEATS
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"Phylogenetic analysis of Ricktsia spp. by comparing sequence 'Phylogenetic analysis of Ricktsia spp. by comparing sequence 'gene D' coding for an intracytoplasmic protein.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
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P24733;
                                                                                                                                                                        TISSUE-Adductor muscle;
MEDLINE-91088319; PubMed-2263488;
Nyitray L., Goodwin E.B., Szent-Gyorgyi A.G.;
"Nucleotide sequence of full length cDNA for muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990).
                                                                                                                                                                                                                                                                                                                                       Nyitray L., Goodwin E.B., Szent-Gyoergyi A.G.; "Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation."; J. Biol. Chem. 266:18469-18476(1991).
Nature
[4]
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                                                        Szent-Gyorgyi A.G., Cohen C. Structure of the regulatory
                                                                                             Xie X., Harrison D.H., Schlichting I.,
                                                                                                                  x-ray Crystallography (2.8 ANGSTROMS) OF MEDLINE=94173332; PubMed=8127365;
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Best Local Similarity 22.2
Matches 87; Conservative
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InterPro; IPR002928; Myosin_tail.
InterPro; IPR002927; Spectrin.
InterPro; IPR001609; Myosin_head.
Pfam; PF00612; IQ; 1.
Pfam; PF00613; Myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PFAINTS; PR00193; MYOSINHBAVY.
PRODOM; PD000355; Myosin_head; 1.
SMART; SM002015; IQ; 1.
SMART; SM002015; IQ; 1.
SMART; SM002015; IQ; 1.
1037 REKKVRGDVEKA-----KRKVEQDLKSTQENVEDLERVKRE-LEENVRRKEAEI---- 1084
                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                              131 KEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAES 190
                                                                                 979
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                           TURN
                                                                                                                                                                                                                                                                                                                                          TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                             925 DEEDAAADLEGIKKKMEADNA-----NLKKDIGDLENTLQKAEQDKAHKDNQISTLQGE 978
                                                                                                                                                                                                                                                                                                                         HELIX
                                                                                                                                                                                                                                                                                                                                                       HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Alkylation; Calmodulin-binding; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the regulatory domain of scallop myosin at 2-A resolution: implications for regulation.";

Structure 4:21-32(1996).
-i- FUNCTION: MUSCLE CONTRACTION.
-i- FUNCTION: MUSCLE CONTRACTION.
-i- FUNCTION: MUSCLE CONTRACTION.
ACTIVATE THAT IS ACTIVATED BY F-ACTIN.
-I- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MIC)
-I- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
-I- SUBLIBRITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-I- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                           74 ---EYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLG 130
                                                                                                                                                            18 DESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHONNGLDT---- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S13557; S13557.
PIR; A40997; A40997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; x55714; CAA39247.1; -.
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PDB; 1WDC; 11-JUL-96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 777-836.
MEDLINE-96419133; PubMed-8805510;
                                                              ISQQDEHIGKLNKEKKALEEANKKTSDSLQAE--EDKCNHLNKLKAKLEQALDELEDNLE 1036
                                                                                                                                                                                                                                                                                     1938 AA;
                                                                                                                                                                                                                                                                                                                                      805
1938
1938
1938
693
703
703
821
                                                                                                                                                                                                                    8.5%; Score 157;
22.2%; Pred. No. 4;
                                                                                                                                                                                                                                                                           222821 MW; A5CCE4127D1A4896 CRC64;
                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                    RODLIKE TAIL (S2 AND LMM DOMAINS).
COLLED COIL (POTENTIAL).
ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYOSIN HEAD-LIKE
                                                                                                                                                                                              Mismatches 166; Indels
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1241 CSEKVMKQFESQMSDLNARLEDSQRSINELQS 1272
                                                                   1193 HODAANEMADQVDQLQKVKSKLEKDKKDLKREMDDLESQ----
                                                                                                                                       1144 GERLDEAGGATSAQIELNKKREAELLKIRRDLEEASLQHEAQ---
                               345 ADE-LEKLFESVKNLSKAAKEMLTNSVKELTS 375
                                                                                                                                                                                      248
                                                                                                                                                                                                                                       191 PAMVNNSGKDGNTSANSADESVK--GPNLTEISKKI-TESNAVVLAVKEVETLLTSIDEL 247
                                                                                               KISAIKDSGELKABIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKG 344
                                                                                                                                                          AKAIGK-------KIKNDV---SLDNEADHNGSLISGAYLISNLITK 284
                                                                                                                                                                                                       SSLNSKLEDEQNLVSQLQRKIKELQARIEELEEELEAERNARAKVEKQRAELNRELEEL 1143
                                                                 ---MTHNMKNKG 1240
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Search completed: March 18, 2002, 10:11:42 Job time: 960 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         526
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1: /cgn2_6/ptodata/2/
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1859
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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    US-08-235-836C-110
US-08-158-353-3
US-08-158-353-3
US-08-29-603E-15
US-09-196-293-15
US-08-235-836C-107
US-08-235-836C-107
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US-08-158-353-4
US-08-158-353-4
US-08-158-353-4
US-08-158-353-11
US-08-235-836C-34
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US-08-355-576-1
US-08-460-309-4
US-08-125-077-4
US-08-125-077-4
US-08-125-077-4
US-08-141-121-4
US-08-135-077-4
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Sequence 110, App
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Sequence 15, Appl
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Sequence 4, Appli
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                                                    Query Match
Best Local Similarity
Matches 229; Conserv
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1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60

Conservative

32;

52.1%;

Score 968.5; DB 4; Pred. No. 5.2e-62; 32; Mismatches 93;

Length 466; Indels 31;

Gaps

9;

RESULT 1 US-08-235-836C-110 US-08-235-836C-110 US-08-235-836C-110 US-08-235-836C-110 Sequence 110, Application US/08235836C Patent No. 6248562el Chimeric Proteins Comprisin TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprisin TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE: Brookhaven National Laboratory. STATE: NY STREET: COUNTRY: Upton STATE: NY STATE: PATENTION DATA: APPLICATION NUMBER: US/08/235,836C FILLING DATE: 29-APR-1994 CLASSIFICATION NUMBER: US 08/148,191 FILING DATE: 29-APR-1994 CLASSIFICATION NUMBER: US 08/148,191 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION: NAME: BOGOSIAN, MATGARTEC RESTORMINICATION INFORMATION: TELEPHONE: (516) 282-3738 INFORMATION FOR SEQ ID NO: 110: SEQUENCE CHARACTERISTICS: LENGTH: 466 amino acids TYPE: amino acid TOPOLOGY: 1inear MOLECULE TYPE: protein US-08-235-836C-110 DESCRIPTION POTES IN STATE MOLECULE TYPE: protein	139.5 7.5 1663 5 PCT-US93-07261-16 138 7.4 1098 4 US-08-923-992A-8 136.5 7.3 1038 4 US-08-961-083-60 135.5 7.3 1104 4 US-08-961-782-4 135.5 7.3 1104 4 US-08-923-992A-6 135.7 7.3 128 4 US-08-923-992A-6 135 7.3 57.3 4 US-08-235-836C-112 134 7.2 376 6 5180810-1 132 7.1 1561 3 US-08-127-499A-23	8 144.5 7.8 1164 4 US-08-92 144 7.7 1713 3 US-08-92 0 144 7.7 1713 5 PCT-US94 1 143 7.7 630 4 US-08-92 2 142.5 7.7 1164 4 US-08-92 3 142 7.6 1507 3 US-08-92 4 142 7.6 1507 3 US-08-92 5 139.5 7.5 1588 5 PCT-US93
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, MOLECULE TYPE: US-08-158-353-3
                                  Ouery Match
Best Local Similarity 97.
Matches 190; Conservative
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; Sequence 3, Application US/08158353
; Patent No. 5620862
; GENERAL INFORMATION:
                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: CAITCIL, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT93-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                    TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: INC
STREET: Lexington
CITY: Lexington
CTATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods for Diagnosing Early Lyme
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, p.c. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 TAEKTTLVVKEGTVTLSKNISKSGE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 ELEKLFESV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 SAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGAD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 KLELKGTSDKNNGSGVLEGVKADKSKVKLTIS----DDLGQTTLEVFKEDGKTLVSKKV 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELTSPYVÄESPKKPKQ-NVSSLD---EKNSVSVDLPGEMKVLVSKEKNKDGKYDLIATVD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELTSPVVABSPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNA--VVLAVK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                                                                       linear
                                                                                                                        protein
                                                                                                                                                  single
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                                                50.8%;
                                                                                                                                                                                                                                                                                                                                           US/08/158,353
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                         Score 945; DB 1;
Pred. No. 8.9e-61;
3; Mismatches 1
                                                Length 210;
                       Indels
                    0;
                  Gaps
               0
                                                                                                                                      CLASSIFICATION 446
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
APPLICATION NUMBER: US 07/862,535
APPLICATION NUMBER: 19-JUN-1992
APPORNEY/AGENT INFORMATION:
ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LIKR-9217-A
TELEPHONE: (212) 697-3355
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
I.FNGTH: 210
               MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: N/A
ANTI-SENSE; N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-209-603E-15
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            ORGANISM: B. E
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Patent No. 6248538
GEMERAL IMPORMATION:
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version
SOFTMARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                        TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PR
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 10-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BROOKS HALLE
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 ELTSPVVAESPKKP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ELTSPVVAESPKKP 194
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17 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
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DSM 5662
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WILSKE, BETTINA
PREAC-MURSIC, VERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTZ, MANFRED
SOUTSCHECK, ERWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/209,603E
10-MAR-1994
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APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettine
APPLICANT: Wilske, Bettine
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.0010S2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-10-06-13
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US-09-196-293-15
; Sequence 15, A
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; PUBLICATION INFORMATION:
US-08-209-603E-15
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                                                                                                                                                                                                                                  ; ORGANISM: Borrella burgdorferi
US-09-196-293-15
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 15
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.5%;
Best Local Similarity 97.4%;
Matches 189; Conservative
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6183755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fuchs, Renate APPLICANT: Motz, Manfred
                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                  KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                    IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
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 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
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                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                          for Windows Version 4.0
                                                                                                                                                            50.2%;
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N/A
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Pred. No. 2.8e-60;
3; Mismatches 2
                                                                                                                                         Score 933; DB 4;
Pred. No. 6.4e-60;
3; Mismatches 1
                                                                                                                                             1; Indels
                                                                                                                                                                            Length 209;
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                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/14/
APPLICATION NUMBER: US 08/14/
APPLICATION NUMBER: US 08/14/
APPLICATION NUMBER: 25,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrella Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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 181
                                                                                                 77
                                                                                                           61 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                           Local Similarity
ELTSPVVAESPKKP 194
                               KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                              IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
                                                                                                                                                                                                                            188;
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                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      282-3729
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                                                                                                                                                                                                                         Score 932; DB 4;
Pred. No. 7.6e-60;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                       Length 210;
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В

197

ELTSPVVAESPKKP 210

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US-08-235-836C-107
; Sequence 107, Application US/08235836C
,; Patent No. 6248562
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                                                                                                                                                                                                                                                                                                                                              Matches 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 122,
                                                                                                                                                                                                                                                                                                                                                                            uery Match
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein 08-235-836C-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-11-93
                                                                                                                                                           406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
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APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins
TITLE OF INVENTION: Borrelia Polypeptides and Uses T
                                                                                              466
                                                                                                           184 SPVVAESPKKPSMVNNSGKDGNTSANSADESVK 216
                                                                                                                                                                                                               346 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 405
                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                          64 KIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                 EKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
                                                                                         SPVVAESPKKPGTMAQYNQMHMLSNKSASQNVR 498
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                                                                                                                                                                                                                                                                                                                                                          50.0%;
89.7%;
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                                                                                                                                                                                                                                                                                                                                                        Score 929; DB 4; Length 588; Pred. No. 4.7e-59;
                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                           Indels
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US-08-158-353-2

; Sequence 2, Application US/08158353
; Patent No. 5620862
; GENERAL INFORMATION:
; APPLICANT: Padula, Steven J.
; TITLE OF INVENTION: Methods for D
TITLE OF INVENTION: Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/23
FILING DATE: 29-APR-1994.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/14.
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Margaret C.
NAME: BOGOSIAN, Margaret C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
  CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: BN TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                          184 SPVVAESPKKP 194
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                                                                                                                                                                                                                                                      456 SPVVAESPKKP 466
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                                                                                                                                                                                                                                                                                                                                               124 EKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (516) 282-3729
TELEPHONE: (516) 282-3729
TELEPHONE: (516) 780-770 TD NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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STATE: NY
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  Brook,
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Smith & Reynolds,
                                                                          Diagnosing Early Lyme
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STREET: CITY: L

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; MOLECULE TYPE:
US-08-158-353-2
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Best Local Similarity
                                                                                                                                                                                                                                                             Sequence 2, Application US/08031295 Patent No. 5530103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                 APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617-861-6240
                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                         178
                                                                                                                                                                                                                                                                                                                                                                                                                    196 SVKELTSPVVAENPKKP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                          COUNTRY:
                                                                                                        CITY: Washington, D.C.
                                                                                                                        STREET:
                                                                                                                                     ADDRESSEE:
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                                                                               ZIP: 20007-5109
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                                                                                                                       E: Foley & Lardner 3000 K Street, N.W.,
                                                                                           USA
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PatentIn Release #1.0,
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                                                                                                                        Suite 500
Version
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; MOLECULE TYPE:
US-08-031-295-2
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US-07-903-580-2
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                                                                                                                                                                                                                                                                                                       Sequence 2, Applic
Patent No. 6221363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AI
TITLE OF INVENTION: PREVENTION
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                           137
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                                                                                                               STREET: 1800 Dia
CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                   COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/727,245 FILING DATE: 11-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MACNNSGKDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS
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                                                                                                                                                                                                                                                                                                                        Application US/07903580
                                                                                                                                                3: Foley & Lardner
1800 Diagonal Road, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
PatentIn Release #1.0,
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22-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.0%;
73.0%;
                                                                                                                                                                                                                     METHOD AND COMPOSITION FOR THE PREVENTION OF LYME DISEASE
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Pred. No. 4.5e-41;
5; Mismatches 36
Version #1.25
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CURRENT APPLICATION DATA:

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                                                                                                                                                                                                                                                                               Sequence 4, Application US/08158353
Patent No. 5520862
GENERAL INFORMATION:
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                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relase #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 143;
                                                                                                                                                                    APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for Diagnosing Early Lyme
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CLASSIFICATION: 435
               APPLICATION NUMBER: FILING DATE:
                                                                                                                               COUNTRY: UZIP: 02173
                                                                                                                                                                  STREET: Two Mili
                                                                                                                                                                                                                                                                                                                                                                                              179 VKELTSPVVAESPKKP 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
TOROTO
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NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/727, 245 FILING DATE: 11-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIGKKIHONNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                        US/08/158,353
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; ORGANISM: Borrelia burgdorferi
US-09-196-293-11
                                                                                                                                                                                                    CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US/09/196,293
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1980-12-22
EARLIER FILING DATE: 1980-12-22
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
NUMBER OF SED ID NOS: 16
SOPTMANDER: ES-450, 65-11
                                                              NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 212
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US-09-196-293-11
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APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
FILE REFERENCE: 738.001US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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Patent No. 6183755
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MACNNSGKDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i: 212 amino acids
amino acid
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linear
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ent No. 6248538:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ON B. BURGDORFERI
                                                      DESCRIPTION: PROHYPOTHETICAL: N/A
ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FUCHS, RENATE APPLICANT: WILSKE, BETTIME
                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: N
STATE:
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIGQKIDNNNGLAALNNONGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WILSKE, BETTINA PREAC-MURSIC, VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOUTSCHECK, ERWIN
                                                                                      PROTEIN
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3; Mismatches 43
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US-08-235-836C-34
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; ORIGINAL SOURCE:
US-08-209-603E-11
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Best Local Similarity
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ZIP: 11973
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equence.
Patent No. 624555.
Patent No. 624555.
GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Borrelia Polypeptides and Uses 7
                                             TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                 NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 01-11-93 AFTORNEY PAGENT INFORMATION:
                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Pred. No. 3.8e-38;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-836C-34

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US-08-235-836C-32
                                                                                 TELEPHONE: (516) 282-7338
TELEFAX: (516) 282-7729
INFORMATION FOR SEO ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-235-836C-32
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Best Local Similarity
                         Query Match
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                                                                                                                                                                                                      APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BN193-28A
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 282-7338
TELEPHONE: (516) 282-7329
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CURRENT APPLICATION UMBER: US/08/235,836C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
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ZIP: 11973
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                                                                                                                                                                                 6) 202
) 282-3729
NO: 32:
   33.1%;
68.2%;
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Score 614.5; DB 4;
Pred. No. 4.1e-37;
               Length 209;
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                                                                                                                                                                                                                  Matches 133;
                 180 KELTSPVVAESPKKP 194
                                            135 NRLKGSHAQLGVAAATDDHAKEAILKSNPTKDKGAKALKDLSESVESLAKAAQEALANSV 194
195 KELTNPVVAESPKKP 209
                                                             120 NKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSV 179
                                                                                                              61 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKN-EGLKEKIDAAKKCSETET 119
                                                                                                  75 IGKVIHQNNGLNANAGQNGSLLAGAYAISTLITEKLSKLKNSEELNKKIEEAKNHSEAFT 134
                                                                                                                                                      17 ISCNNSG--GDTASTNPDESAKGPNLTVISKKITDSNAFVLAVKEVEALISSIDELANKA 74
                                                                                                                                                                   Conservative
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Search completed: March 18, 2002, 09:55:32 Job time: 345 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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1859
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/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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score greater than or equal to the score of the result being and is derived by analysis of the total score distribution No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed.

SUMMARIES

Result
Score
Query Match
Length DB
10
Description

5.5.5 400 19 US-09-596-746-40 373 19 US-09-596-746-40	85.5 400 19 US-09-596-746-82 Sequence 84.2 374 19 US-09-596-746A-26 Sequence 84.2 374 19 US-09-596-746A-26 Sequence 84.0 373 19 US-09-596-746A-26 Sequence 83.8 398 19 US-09-596-746A-62 Sequence 82.5 371 19 US-09-596-746A-62 Sequence 82.1 394 19 US-09-596-746A-64 Sequence 82.1 394 19 US-09-596-746A-64 Sequence 82.1 395 19 US-09-596-746A-64 Sequence 82.1 395 19 US-09-596-746A-78 Sequence 80.4 369 19 US-09-596-746A-78 Sequence 80.3 409 19 US-09-596-746A-78 Sequence 80.3 409 19 US-09-596-746A-78 Sequence 80.1 368 19 US-09-596-746A-78 Sequence 80.1 368 19 US-09-596-746A-72 Sequence 69.1 369 19 US-09-596-746A-72 Sequence 69.1 369 19 US-09-596-746A-56 Sequence 69.1 369 19 US-09-596-746A-56 Sequence 69.1 369 19 US-09-596-746A-66 Sequence 67.2 368 19 US-09-596-746A-66 Sequence 68.9 394 19 US-09-596-746A-66 Sequence 66.8 392 19 US-09-596-746A-66 Sequence 66.8 392 19 US-09-596-746A-8 Sequence 65.3 378 19 US-09-596-746A-8 Sequence 65.0 394 19	4	_	ω	N	1	0	9	œ	7	0	G	4	w	N	س	0	9	8	7	σ	u	4	w	N	سر	20 1	9	8	7	6	ഗ	4	ω	N	_	c
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19 US-09-596-746A-28 19 US-09-596-746A-28 19 US-09-596-746A-26 19 US-09-596-746A-36 19 US-09-596-746A-36 19 US-09-596-746A-36 19 US-09-596-746A-36 19 US-09-596-746A-46 19 US-09-596-746A-47 19 US-09-596-746A-78 19 US-09-596-746A-79 19 US-09-596-746A-79 19 US-09-596-746A-6-79	00 19 US-09-596-746-82 Sequence 74 19 US-09-596-746A-82 Sequence 74 19 US-09-596-746A-82 Sequence 75 19 US-09-596-746A-26 Sequence 76 19 US-09-596-746A-62 Sequence 77 19 US-09-596-746A-64 Sequence 78 19 US-09-596-746A-64 Sequence 79 19 US-09-596-746A-64 Sequence 79 19 US-09-596-746A-64 Sequence 70 19 US-09-596-746A-78 Sequence 70 19 US-09-596-746A-78 Sequence 70 19 US-09-596-746A-78 Sequence 70 19 US-09-596-746A-79 Sequence 70 19 US-09-596-746A-72 Sequence 70 19 US-09-596-746A-72 Sequence 70 19 US-09-596-746A-72 Sequence 70 19 US-09-596-746A-73 Sequence 70 19 US-09-596-746A-74 Sequence 70 19 US-09-596-746A-68 Sequence 70 19 US-09-596-746A-69 Sequence 70 19 US-09-596-746A-69 Sequence 70 19 US-09-596-746A-69 Sequence 71 19 US-09-596-746A-69 Sequence 72 US-09-596-746A-69 Sequence 73 19 US-09-596-746A-69 Sequence 74 19 US-09-596-746A-69 Sequence 75 19 US-09-596-746A-69 Sequence 76 19 US-09-596-746A-69 Sequence 77 US-09-596-746A-69 Sequence 78 19 US-09-596-746A-69 Sequence 79 US-09-596-746A-69 Sequence 79 US-09-596-746A-69 Sequence 70 US-09-596-746A-69 Sequence 70 US-09-596-746A-69 Sequence 71 US-09-596-746A-69 Sequence 72 US-09-596-746A-69 Sequence 73 US-09-596-746A-69 Sequence 74 US-09-596-746A-69 Sequence 75 US-09-596-746A-69 Sequence 76 US-09-596-746A-69 Sequence 77 US-09-596-746A-69 Sequence 78 US-09-596-746A-69 Sequence 79 US-09-596-746A-69 Sequence 79 US-09-596-746A-69 Sequence 79 US-09-596-746A-69 Sequence 79 US-09-596-746A-69 Sequence 70 US-09-596-746A-69 Sequence 70 US-09-596-746A-69 Sequence 71 US-09-596-746A-69 Sequence 72 US-09-596-746A-69 Sequence 73 US-09-596-746A-69 Sequence 74 US-09-596-746A-69 Sequence 75 US-09-596-746A-69 Sequence 76 US-09-596-746A-69 Sequence	٠.	л	ū	Ġ	ū	ū	5	Ġ	ġ	7.	7.	œ	œ	9	9	.8	œ	0	0	0	0	0	0	0	0	Ñ	N	N	N	ü	Ü	4	4	Ġ	Ġ	ċ
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ALIGNMENTS

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; FEATURE:
; OTHER INFORMATION: OSPC Chimera
US-09-596-746-28
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                                                                                                                                                                                                                                                                                                      APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 199-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/09596746 GENERAL INFORMATION:
  Query Match
Best Local Similarity
Matches 378; Conserv
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APPLICANT:
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                        LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dattwyler, Raymond J.
Seinost, Gerald
100.0%; Score 1859; DB 19; ilarity 100.0%; Pred. No. 4.5e-123; Conservative 0; Mismatches 0;
                                                       Length 378;
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Best Local Similarity 100.
Matches 378; Conservative
       181 ELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV 240
                                        121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                    121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                61 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETN 120
                                                                                             61 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Applica GENERAL INFORMATION:
                                                                                                                          1 MACNNSGKDGNTSANSADESVKGDNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                                                                      1 MACNUSGRDGUTSANSADESVKGPULTEINKKITDSNAVLLAVKSVEALLSSIDEIAAKA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 EIEKAKKCSBEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFEGVKN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ETLLTSIDELAKAIGKKIKNDYSLDNEADHNGSLISGAYLISNLTTKKISAIKDSGELKA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KLKEKHTDLGKEGVTDADAKBAILKANGTKTKGAEELGKLEESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLEESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                               100.0%; Score 1859; DB 19,
100.0%; Pred. No. 4.5e-123;
0; Mismatches 0;
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US-09-596-746-80
385 SKAAKEMLTNSVKELTS 401
             362 SKAAKEMLTNSVKELTS 378
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              325 IEKAKKCSBEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNL 384
                            302 IEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNL 361
                                                        265 TLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE 324
                                                                    242 TILTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE 301
                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                205 LTSPVVAESPKRPSMVNNSGKOGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 264
                                                                                                            182 LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 241
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US-09-596-746-80
; Sequence 80, Application US/09596746
; GENERAL IMPORMATION:
                                                                                                                                          145 LKEKHTDLGKEGVTDADAKEAILKTNGTKTKGABELGKLFESVEVLSKAAKEMLANSVKE 204
                                                                                                                                                      122 LKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLEESVEVLSKAAKEMLANSVKE 181
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dybhulzen, Danial APPLICANT: Lift, Benjamin J.
TITLE OF INVENTION: Groups of Borrelia burgdorferi and CURRENT E111.02-101. 1002-001 afzelii That Cause Lyme Disease in Humans CHRENT APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: US/09/596,746
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
SOFTWARDE. SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                  85 GKKIHONNGLDTEYNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNK 144
                                                                                                                                                                                              62 GKKIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNK 121
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Soleck
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173; Conservative
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98.9%; Pred. No. 2.9e-121;
tive 2; Mismatches 2; Indels 0
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US-09-596-746A-80

Sequence 80, Application US/09596746A GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.

APPLICANT:

Seinost, Gerald

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Sequence 24, Application US/09596746A
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-66-19
PRIOR APPLICATION NUMBER: US 60/140,042
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SEQ ID NO 80
LENGTH: 402
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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Best Local Similarity 98.9
Matches 373; Conservative
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9-596-746A-80
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                                                                                                                                                                                                                                                                                                                                                    402
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Pred. No. 2.9e-121;
Pred. No. 2.9e-121;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Setnost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme D
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 199-06-18
NUMBER OF SEQ ID NOS: 84
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; OTHER INFORMATION: OSPC Chimera US-09-596-746-24
                                                                           SOFTWARE: FE
SEQ ID NO 24
LENGTH: 374
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NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/09596746 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                              FastSEQ
                                                                                                               for Windows Version 4.0
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98.1%;
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Pred. No. 1.2e-119;
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Lyme Disease
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APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
FILE REFERENCE: 2631,1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
RIOR APPLICATION NUMBER: US 60/140,042
RIOR FILING DATE: 1999-06-18
SOFTMARE: FastSEQ for Windows Version 4.0
I.FNGTH: 308
                                                                                                                                                                                                                                                                                                   ; ORGANISM: ospC Chimera
US-09-596-746-60
                                                                                                                                                                                                                             Matches 369;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                         62 GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETNK 121
                                                                                                                                                 25 SCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI 84
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nes 370; Conservative
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                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                            97.0%; Score 1802.5; DB 19; Length 398; 97.9%; Pred. No. 4.8e-119; Indels 3; Mismatches 2; Indels 3;
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SEQ ID NO 60
LENGTH: 399
TYPE: PRT
ORGANISM: OSPC Chimera
US-09-596-746A-60
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US-09-596-746A-60
; Sequence 60, Application US/09596746A
; GENERAL INFORMATION;
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Seinost, Gerald
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
; TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
; FILE REFERENCE: 2631,1002-001
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383 SKAAKEMLTNSVKELTS
                                                                                                                         242 TLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE
                                                                                                                                                                                  182 LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE 241
                                                                                                                                                                   206 LTSPVVAES---PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVE
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                   SKAAKEMLTNSVKELTS 378
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369; Conserv
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Pred. No. 4.8e-119;
3; Mismatches 2; Indels 3;
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Gaps

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US-09-596-746-30

Sequence 30, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald

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US-09-596-746A-30
(Sequence 30, Application US/09596746A
(Sequence 30, Application US/09596746A
(GENERAL INFORMATION:
(APPLICANT: Dattwyler, Raymond J.
(APPLICANT: Selnost, Gerald
(APPLICANT: Selnost, Gerald
(APPLICANT: Luft, Benjamin J.
(APPLICANT: Matia J.C. Gomes-Solecki
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LENGTH: 377
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 331; Conserv
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CURRENT APPLICATION NUMBER: US/09/596,746

CURRENT FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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NUMBER OF SEQ ID NOS:
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87.8%; Pred. No. 9e-106;
tive 20; Mismatches 2
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                                                             Disease
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FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEO ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 30
LENGTH: 377
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; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-30
US-09-596-746-82
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                                                           SOFTWARE:
SEQ ID NO 82
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APPLICANT:
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                                                                                       APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D1
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS. 84
                               LENGTH: 4
TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                             FastSEQ
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                                                                               for Windows
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Pred. No. 9e-106;
                                                                               Version
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US-09-596-746A-82
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US-09-596-746A-82
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FILE REFERENCE: 2631.1002-001
FURRENT APPLICATION NUMBER: US/09/596,746A
FURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 199-06-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82
LENGTH: 401
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                                                                                                                                                                                                 Query Match
Best Local :
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Best Local Similarity
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                                                          62 GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNK 121
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LKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE 181
                                             GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK
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                                                                                                                                                                             Conservative
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86.7%; Pred: No. 5.8e-104;
Mismatches 27;
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86.7%; Pred. No. 5.7e-104;
tive 22; Mismatches 27; Indels
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; OTHER INFORMATION: OspC Chimera US-09-596-746A-26
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US-09-596-746A-26
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SEQ ID NO 26
LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT:
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APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gones-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631,1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SECID NOS: 84
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                  ABIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK
ETLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLK
                                                                           ETLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK
                                                                                                                   ELTSPVVAES----PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI
                                                                                                                                  ELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV 240
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US-09-596-746-26

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APPLICANT: Dattwyler, Raymond J.

APPLICANT: Selnost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in I
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US 60/140,042
MINDER OF SEQ ID NOS: 84
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SEQ ID NO 26
LENGTH: 373
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Best Local Similarity
Matches 323; Conserv
                                         Sequence 62, Application US/09596746 GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
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LAKAAKEMLANSVKEL 373
                                                                                                                                                                               GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
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 Dykhuizen, Danial
             Dattwyler, Raymond J.
Seinost, Gerald
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85.9%; Pred. No. 5.4e-102;
tive 22; Mismatches 27;
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Search completed: Job time: 971 sec

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62

LENGTH: 397

TYPE: PRT
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Best Local 9
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeiii That Cause Lyme Disease in |
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
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                                                                     301 EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
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85.6%; Pred. No. 9.6e-102;
tive 23; Mismatches 27;
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1: /ggn2_6/ptodata/2/paa/PCT_NEW_COMB.pep

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pe

3: /ggn2_6/ptodata/2/paa/USO9_NEW_COMB.pe

4: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pe

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pe

6: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pe

7: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pe

8: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pe
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    303921 segs, 63882009 residues
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US-09-708-427-19883
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US-09-815-242-5835
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US-09-918-275-7
US-09-938-275-7
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19883, A
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MACNISGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEZ ::	US/09974992 Marianne J. ichael ichael , Soren vel OspC-derived peptide fragments 6p 2001-10-10 ER: 09/180,089 9-05-13 9-05-13 9-05-02 40 10-05-02 40 17.0%; Score 692.5; DB 6; Leng 17.0%; Pred. No. 8.6e-40; tive 12: Mismatches 30; Inde	26 156 8.4 1144 6 US-09-708-427-15046 27 155.5 8.4 690 5 US-09-748-875-61 28 155.5 8.4 691 5 US-09-748-875-61 29 155.5 8.4 691 5 US-09-748-875-62 30 155.5 8.4 701 5 US-09-748-875-62 31 155.5 8.4 701 5 US-09-748-875-62 32 155.5 8.4 702 5 US-09-748-875-62 33 155.5 8.4 929 5 US-09-708-427-21161 34 155 8.3 1703 6 US-09-708-427-21160 35 155 8.3 1740 6 US-09-708-427-21159 36 151.5 8.1 2086 6 US-09-708-427-2159 37 151.5 8.1 2086 6 US-09-815-242-5639 38 151.5 8.1 5795 6 US-09-815-242-15610 39 151.5 8.1 5795 6 US-09-815-242-15610 40 148 8.0 1690 6 US-09-614-150-10224 41 148 8.0 1690 6 US-09-614-150-10224 42 148 8.0 2056 6 US-09-614-150-10224 43 148 8.0 3070 6 US-09-614-150-10224 44 148 8.0 3070 6 US-09-614-150-10224 45 147.5 7.9 1639 6 US-09-614-150-08213
ALLSSIDEIAAKA		Sequence 1 Sequence 2 Sequence 6 Sequence 6 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 1 Sequence 2 Sequence 2 Sequence 3 Sequence 4 Sequence 4 Sequence 6 Sequence 7 Sequence 7
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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR APPLICATION NUMBER: PCT/DK97/00203
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
LENGTH: 212
TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-974-992-7
                                                                                              : SEQ ID NO 3
LENGTH: 207
: TYPE: PRT
: ORGANISM: Borrelia garinii
US-09-974-992-3
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                     Query Match
Best Local Similarity
              Matches 128;
                                                                                                                                                                                                                                                              APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 69.9%;
Matches 137; Conservative 1
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mathiesen, Marianne J. APPLICANT: Theisen, Michael
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APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERNCE: 459-666P
                                                                                                                                                                                                                                                                                                                                                                                                                     quence 3, Application US/09974992
NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mathiesen, Marianne J. APPLICANT: Theisen, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 TNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
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          Conservative
                       32.1%;
        25;
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                       Score 596.5; DB (
Pred. No. 2.5e-33;
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     Mismatches
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                                 DB 6;
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   Indels
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: LOCATION: (1881)..(1881)
: OTHER INFORMATION: X=any amino
US-10-032-585-764
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Best Local Similarity
Matches 100; Conserv
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IITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
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              1746
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ORGANISM: Candida albicans
FEATURE:
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LQFLSGNKSKELEDYIQK----HSDISEKLKALTDELKEKTKQFDDSKKKLTELENDLTS 1801
                                                                                                          --KIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA-----EIEKAK-- 306
                                                                                                                                                    TSIEE - - KNNQIKELSETIKSLKTELKTSGDALKQSQKEYKTLKTKNSDTESKLEKQLEE
                                                                                                                                                                                    NSADESVKGPNLTEISKKI-----TESNAVVLAVKEVETLLTSIDELAKAIGK----
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                                                                          LEKVKSDLQTADE-KLKGITEREIALKSELETVKNSGLSTTSELAALTKTVKSLEKEKEE
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                                    -KCSEEFTAKLKGEHTDLGK--EGVTD------DNAKKAILKTNNDKTK 346
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Pred. No. 0.0025;
'8; Mismatches 171;
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; LOCATION: (1881)..(1881)
; OTHER INFORMATION: X=any amino acid
US-10-072-851-15590
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US-10-072-851-15590
; Sequence 15590, Application US/10072851
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Best Local :
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15590
LENGTH: 1881
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TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TILE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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                                 1687 LEKVKSDLQTADE-KLKGITEREIALKSELETVKNSGLSTTSELAALTKTVKSLEKEKEE 1745
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   307
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                                                                                                   TSIEE--KNNQIKELSETIKSLKTELKTSGDALKQSQKEYKTLKTKNSDTESKLEKQLEE 1686
                                                                                                                                 NSADESVKGPNLTEISKKI-----TESNAVVLAVKEVETLLTSIDELAKAIGK----
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Yamar, Terry
   -----KCSEEFTAKLKGEHTDLGK--EGVTD----
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Zyskind, Judith W
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Boone, Charles
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Yamamoto, Robert T.
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Zamudio, Carlos
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21.0%; Pred. No. 0.0025;
tive 78; Mismatches 171;
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 -----DNAKKAILKTNNDKTK 346
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Best Local Similarity
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TYPE: PRT
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; LOCATION: 1..1313;
OTHER INFORMATION: Xaa is any ami;
NAME/KEY: misc_feature
; LOCATION: 1..1313;
OTHER INFORMATION: Ceres Seq. ID
US-09-708-427-15044
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GENERAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: US/09/708,427

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 15044
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NAME/KEY: misc_feature
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KATLLVCQEELKNC---ESQVDSLKLASKETNEKYEKMLEDARNEIDS 486
                                                                 KAILKTNNDKTKGADELEKLFESVKNLSKAAKE----MLTNSVKELTS 378
                                                                                                                                                                    ISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAK 334
                                                                                                                                                                                                                                                                                                                              VKEVETLLTSIDE------LAKAIGKKIKNDV--------
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                                                                                                                                  -----IQNLLDQRTELSIELERCKVEEEKSKKDMESLTLAL-----QEASTESSEA 441
                                                                                                                                                                                                                                                             EKTIEAQRTDLEEYGRQVCIAKEEASKLENLVESIKSELEISQEEKTRALDNEKAATSN- 395
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.1304
OTHER INFORMATION: Xaa is any amino ac
NAME/KEY: misc_feature
LOCATION: 1.1304
COCATION: 1.1304
OTHER INFORMATION: Ceres Seq. ID 18286
                 RESULT 8
US-09-708-427-19883
; Sequence 19883, Application
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US-09-708-427-15045
Sequence 15045, Application US/09708427
SEQUENCE 15045, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
FITTLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FITTLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
FILE REFERENCE: 2750-1243P
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 15045
LENGTH: 1304
TYPE: PRT
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                                                                                                                                           LEKLFESVKNLSKAAKE----MLTNSVKELTS
                                                                                                             -ESQVDSLKLASKETNEKYEKMLEDARNEIDS
                                                                                                                                                                   LSIELERCKVEEEKSKKDMESLTLAL-----QEASTESSEAKATLLVCQEELKNC--
                                                                                                                                                                                                AIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADE
                                                                                                                                                                                                                               QVCIAKEEASKLENLVESIKSELEISQEEKTRALDNEKAATSN-----IQNLLDQRTE
                                                                                                                                                                                                                                                            ---LAKAIGKKIKNDV------SLDNEADHNGSLISGAYLISNLITKKIS 290
                                                                                                                                                                                                                                                                                         KSŚASEŚME-----SVMKQLAELNHVLHETKSDNAAQKEKIELLEKTIEAQRTDLEEYGR
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                                      US/09708427
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
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US-09-708-427-19882

Sequence 19882, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOSTWARE: Patentin version 3.1
SEQ ID NO 19883
LENGTH: 1014
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
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Best Local Similarity 23.1%;
Matches 113; Conservative 7
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THERBBY
FILE REFERENCE: 2750-1243P
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OTHER INFORMATION: Xaa is
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; LOCATION: 1..1018
; OTHER INFORMATION: Xaa is :
; NAME/KEY: misc_feature
; LOCATION: 1..1018
; OTHER INFORMATION: Ceres S
US-09-708-427-19882
                                                                       Sequence 19881, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-12439

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 83364

SOFTWARE: Patentin version 3.1
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Matches 113; Conserv
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SOFTWARE: PatentIn version
SEQ ID NO 19882
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Best Local :
                                                           SEQ ID NO 19881
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ORGANISM: Arabidopsis thaliana
                     TYPE: PRT
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; LOCATION: 1.1269
; OTHER INFORMATION: Ceres
US-09-708-427-19881
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                                                                                                                                                                                                                                                                                              Sequence 5883, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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Best Local
                                                                                                 APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yu. Howard

TITLE OF INVENTION: Identification of Essential Genes

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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OTHER INFORMATION: Xaa
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                      Sequence 5883, Application GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5883
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APPLICANT:
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                APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
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Best Local :
     CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                       Carr, Grant J.
                                                                                     Jiang, Bo
Boone, Charles
                                                                                                                        Roemer,
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Zamudio, Carlos
Haselbeck, Robert
                                                                                                                                                           Trawick, John D.
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                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W
                                                                                                                                          Yamamoto,
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NUMBER: US/10/072,851
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18.7%;
                                                                                                                                            Robert T
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5883
LENGTH: 837
TYPE: PRT
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Best Local :
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671 AAKQALNGNANVQHAKDEATALINSSNDLNQAQKDALKQQVQNATT
                                     333
                                                                   611 LKQAIADKDATKATVNFTDADQAKQQAYNTAVTNAENIISKANGGNATQAEVEQAIKQVN 670
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18.7%;
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Nicmatches 181;
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US-09-815-242-13080
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APPLICANT:
                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                      PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
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CURRENT FILING DATE: 2001-03-21
                     PRIOR
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APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
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Yamamoto, Robert T.
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

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Best Local Similarity
Watches 76; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13080
LENGTH: 875
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                            APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITER.028A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT FILING DATE: 2002-08-08
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                                                                                                                                                                                         Jiang, Bo
Boone, Charles
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Yamamoto, Robert T
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Zyskind, Judith W.
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Zamudio, Carlos
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                                                                                                                                                                                                                                                                                                  Daniel
                                                                                                                                                                                                                                        Terry
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; LENGTH: 875
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-072-851-13080
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                                                                                                                                                                                                                                                               556
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708
                                          333 AKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTS
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                                                                                                                              288 KISAIKDSGELKAEI-----EKAKK------CSEEFTAKLKGEHTDLG--KEGVTDDN 332
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Local Similarity 18.7%;
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AAKQALNGNANVQHAKDEATALINSSNDLNQAQKDALKQQVQNATT
                                                                                                                                                                                                                TESNAVVLAVKEVETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITK 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Mismatches 181;
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US-09-815-242-5835 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23 GENERAL INFORMATION Sequence 5835, PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308 CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21 TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes APPLICANT: Haselbeck, Robert NUMBER OF SEQ ID NOS: 14110 FILE REFERENCE: ELITRA.011A APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: PRIOR FILING DATE: APPLICANT: APPLICANT: FastSEQ Trawick, John D. Carr, Grant J. Yamamoto, Robert T. Wall, Daniel Xu, H. Howard Zyskind, Judith W. Application US/09815242 for Windows Version 2001-02-16 of Essential Genes 'n

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2323 EQAIKQVNAAKQALNGNANVQHAKDEATALINSSNDLNQAQKDALKQQVQNATT 2376
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                                                                               2263 NLNTAMGNLKQAIADKDATKATVNFTDADQAKQQAYNTAVTNAENIISKANGGNATQAEV 2322
                                   325 KEGYTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 378
                                                                                                                                                                                                                                                                                                                                             148 GTKT--KGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAESPKKPSMVNN----SG 201
                                                                                                                  280 LISNLITKKISAIKDSGELKAEI-----EKAKK-----CSEEFTAKLKGEHTDLG-- 324
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Search completed: March 18, 2002, 09:58:19

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000	Borr	elia bur	gdorfer	i (Lyme	disease spiroche	chete).	
28	Bact	eria; Sp _TaxID=1	irochae 39;	tales;	Spirochaetacea	ae; Borrelia.	
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van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

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Nature 390:580-586(1997).

-!- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
-!- FUNCTION: ATTACHED TO THE OUTER MEMBRANE
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-!- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94075528; PubMed=8253951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKELTSPVVAESPKKP
                                                                                                                                                                                                                                                                                                                                                                                                              TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
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137; Conserv
FROM N.A
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eel. 27, Last senotation update)
eel. 28, Last annotation update)
eel. 28, Last annotation 24
                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                         212
                                                        Spirochaetaceae;
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Pred. No. 2.6e
15; Mismatches
                                                                                                                                                                                                                                      PRT;
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.6e-22;
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                                                      Borrelia
                                                                                                                                    PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY). CRC64;
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Best Local S
Matches 91
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InterPro; IPR001800; L1DUF-
Pfam; PF01441; L1poprotein_6; 1.
ProDom; PD001149; L1poprotein_6; 1.
PROBABLE PS00013; PROBABLE PROBABLE MAJOR OF
                                                                                                                                                               01-JUL-1993
01-JUL-1993
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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Mol. Microbiol. 6:3299-3311(1992).

-!- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                                                                                                                 BORHE
            STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
Restrepo B.I., Kitten T., Carter
                                        SEQUENCE FROM N.A. STRAIN-SSP. HS1 SE
                                                                             Bacteria; Spirochaetales;
NCBI_TaxID=140;
                                                                                                                                               Ol-JUL-1993 (Rel. 26, Created)
Ol-JUL-1993 (Rel. 26, Last sequence update)
Ol-FEB-1994 (Rel. 28, Last annotation update)
VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR
                                                                                                                                                                                                      002448;
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"Subtelomeric expression regions of Borrelia hermsii linear plasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SSP. HS1 SEROTYPE 24; MEDLINE-93133110; PubMed-1484486;
                                                                                                            Plasmid
                                                                                                                       Borrelia hermsii
                                                                                                                                     VMP3.
                                                                                                                                                                                                                   VM03_BORHE
Restrepo B.I., Kitten T., Carter C.J., Subtelomeric expression regions of Bo
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                                                                                                                                                                                                                                                                                                                                           VKSKAEAFLNKLKDGHTELGKKDASDDDTKKAIKKDNSDKTKGASELEALNTAVDALLKA
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214 /
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22541 MW;
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                                                                                            Spirochaetaceae;
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Pred.
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 Borrelia
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               Infante D., Barbour A.G.;
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                                                                                              Borrelia
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hermsii linear plasmids
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
           Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;

"Complete nucleotide sequence and deduced polypeptide
nonmuscle myosin heavy chain gene from Acanthamoeba:
hinge in the rodlike tail.";
J. Cell Biol. 105:913-925(1987).
-I-FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACT
ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-I-SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentitles requires a license agreement (See http://www.isb-sib.ch/amor or send an email to license@isb-sib.ch).
                                                                                                                                                                      Acanthamoeba castellanii (Amoeba) Eukaryota; Acanthamoebidae; Acanthamoebidae; Acant
                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
MYOSIN II HEAVY CHAIN, NON MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pram; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are highly polymorphic.";
Mol. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE
FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                            MEDLINE-87308395; PubMed=3040773;
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         MYSN_ACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -AKAIGKKIKNDNSNFEDENDHNGSLIAGVFQVILTVKAKLTSLEQIIGISDELKTEVGM
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Pred. No. 7.1e
35; Mismatches
                                                                                                                                                                                        Acanthamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-ACYL DIGLYCERIDE 684C74D35F87C771
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VARIABLE MAJOR OUTER MEMBRANE
                                                                                                                                                                                                                                                                                           PRT;
 HEAVY CHAIN
                                                                                     deduced polypeptide sequence from Acanthamoeba: evidence
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SUBUNITS
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                IT SELF-ASSEMBLES
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Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00048; IQ.
InterPro; IPR001609; myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
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SEQUENCE
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DOMAIN 1 789 MYOSIN HEAD-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00624; CAA68663.1; -. PIR; A27224; A27224. HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                       934 ELQEETSASNDILEQKRKLEAEKGELKASLEE---EERNRKALQEAKTKVESERNELQDK 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50096; IQ; Myosin; Coiled coil; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed.
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KSKLSAAEKSLKTAKDQNRDLDEQLEDERTVRANVDKQKKALEAKLTELEDQVTALDGQK 1166
                                           ----VAESPKKPSMVNNSG-----KDGNTSANSADESVKG--PNLTEISKKIT----ES
                                                                                             DDVTATKLQLEKTKKSLEEELAQTRAQLEE-EKSGKEAASSKAKQLGQQLEDARSEVDSL
                                                                                                                                           -DAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPV------
                                                                                                                                                                                           YEDEAAAHDSLKKKEEDLSRE-LRETKDALADAENISETLRSKL--KNTERGADDVRNEL 104
                                                                                                                                                                                                                                       LAGAYAISTLIKQKLDGLKNEGLKEKIDA---AKKCSETFTNKLKEKHTDLGKEGVTDA- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.

MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                     EINKKITDSNAVLLAVKEVEA----LLSSIDEIAAKAIGKKIHQ--NNGLDTENNHNGSL
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SM00242; MYSC;
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Pred. No. 0.33
69; Mismatches
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ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
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COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
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ACTIN-BINDING.
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NONHELICAL TAILPIECE.
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          637
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z70690; CAA94624.1; -. Hypothetical protein. SEQUENCE 1957 AA; 222785
                                        232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q10411;

Q10411;

01-0CT-1996 (Rel. 34, Created)

01-0CT-1996 (Rel. 34, Last sequence update)

01-0CT-1996 (Rel. 34, Last annotation update)

HYPOTHETICAL 222.8 KDA PROTEIN C1F3.06C IN CHROMOSOME

SPACIF3.06C.
                                                                                                                  534 LNELKGELQTEISNSEHLSSQLSTLAAEKEAAVATN-----NELSESKNSLQTLCNAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896;
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SKLQQLQLERANFEQKESTLSDENNDLRTKLLKLEESNKSLIKKQEDVDSLE---
                                   AVVLAVK----
                                                         QEKLAKSVMQL-----KENEQNFSSLDTSFKKLNESHQELEN-----NHQTITKQLKDTS
                                                                                     KEMLANSVKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESN
                                                                                                                                                                                                                                   DKMVKQVSSQLEEARSSLAHATGKLAEINSERDFQNKKIKDFEKIEQDLRACLNSSSNEL
                                                                                                                                                                                                                                                                                            KDSRTSNSQLEEEMVELKESNRT·IHSQLTDAESKLSSFEQENKSLKGSIDEYQNNLSSK 418
                                                                                                                                                                                                                                                                                                                        KDGNTSANSADE----SVKGPNLTEINKKITDSNAVLLAV-KEVEALLSSIDEI-----
                                                                                                                                                                          KEK---SALIDKKDQELNN--LREQIKEQKKVSESTQSSLQSLQRDILNEKKKHEVYESQ
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                     -----TDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAA 171
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22.8%;
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                                                                                                                                                                                                                                                                                                                                                                           Score 173.5;
Pred. No. 0.
                              EVETLLTSIDELAKAIGKKIKNDVSLDNEADHNGS
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                                                                                                                                                                                                                                                                                                                                                          148;
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                                                                                                                                                                                                                                                                                                                                                       Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                     Length 1957;
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Hollingshead S.K., Fischettl V.F., Scott J.R.;
"Complete nucleotide sequence of type 6 M protein of the
Streptococcus. Repetitive structure and membrane anchor."
J. Biol. Chem. 261:1677-1686(1986).
                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                  PRINTS; PRO0015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                              EMBL; M11338; AAA26920.1; -. PIR; A26297; A26297. InterPro; IPR001899; Gram_pos_anchor. InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
"Relationship of M protein genes in group A streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985)
-I- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERVICE OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
M PROTEIN, SEROTYPE 6 PRECURSOR.
                                                                                                                CHAIN
                                                                                                                               SIGNAL
                                                                                                                                           Transmembrane;
                                                                                                                                                         Virulence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85166224; PubMed=3885219;
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                           DOMAIN
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                                                                                                                                                                                                                                                                                                    send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PRO IN THE REGION OF THE MEMBRANE ANCHOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHAGOCYTOSIS.
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                                                                                                                                                                                                               PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                   PF02370; M;
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ane; Coiled co
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                                                                                                                                        Cell wall;
il; Signal.
                        MEMBRANE ANCHOR.
CYTOPLASMIC (POTENTIAL).
10 X 7 AA TANDEM REPEATS.
4.5 X 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMINO
            BLOCKS
                                                                                                  EXTRACELLULAR
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            SEPARATED
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             ВУ
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            15 AMINO
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Best Local
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P19401;
P19401;
Ol-NOV-1990 (Rel. 16, Last sequence update)
Ol-NOV-1990 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).
                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS24 / Serotype M12;
MEDLINE=88058777; PubMed=2445730;
Robbins J.C., Spanier J.G., Jones
Robbins J.C., Spanier J.G., Jones
                                                                                                               J. Bacteriol. 169:5633-5640(1987).

-i- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERVING OF PROTEIN M. PROTEIN M. IS CLOSELY ASSOCIATED WITH VIRULENCE THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                     sequences."
                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                   M12_STRPY
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                                                              SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AN
IN THE REGION OF THE MEMBRANE ANCHOR.
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                                                                            AND STAPHYLOCOCCAL PROTEINS
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Best Local 9
                                                              SCA4_RICAK STANDARD; PRT; 998 AA. (9ALX9; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ANTIGENIC HEAT-STABLE 120 KDA PROTEIN (PS120)
                           Rickettsia akari
                                                (PROTEIN PS 120) (FRAGMENT). SCA4 OR D.
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                                                                                                                                                                                                                                                                                                                                                                  TDDNAKKAILKTNNDKTKGADELEKLFESVKNL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSLEQQLAVTKENAKKDFELAALGHQLADKEYNAKIAELESKLADAKKDFELAALGHQHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKLGIDNADLKAK----TTELEKSYEEKNDVLSQIKKELEEAEKDIQ-----FGREVHAA
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62904 MW;
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22.9%; Pred. No. 0.32;
tive 59; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                 -KKOVEKDLANLTAELDKVKEEKOISDASRQGLRRDLDASRE
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COILED COIL (POT:
GLY/PRO-RICH (CE:
CONSERVED IN GRAJ
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IN GRAM-POSITIVE COCCI
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                                                                  (120 KDA ANTIGEN)
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   RESULT 10
RBP2_PLAVB
ID RBP2_P
AC Q00799
DT 01-APR
DT 01-APR
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Q00799;
01-APR-1993
01-APR-1993
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Query Match 9.0%; Score 167.5; D
Best Local Similarity 20.7%; Pred. No. 0.67;
Matches 102; Conservative 69; Mismatches
848 DISKIAIEKVNN
                                         360
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                                                                                                                                                          755
                                                                                                                                                                         255 GKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEETA 314
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                                                                                                                                                                                                                                                                                                                                                        207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetic analysis of Rickettsia spp. by comparing sequence gene D' coding for an intracytoplasmic protein.", Submitted (DEC-199) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF213016; AAK30691.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=786;
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                                     NLSKAAKEMLTN 371
                                                           GLKGQNLDEPKP--RDDIYNKAQDIAYALKNVVTTVLDANPEKREVSEBEVMNKTSSILN
                                                                                                         KLKGEHTDLGKEGVTDDNAKKA-----
                                                                                                                                                        SKGVDN-----
                                                                                                                                                                                                                  ASHRTMAPTKKIAAIESVETGVAKSITDLEDKKLMTKGLVDGIYEDKANPEITSEMMKAV
                                                                                                                                                                                                                                                                                              AFNTIAKTAAIQKYTTKVLDSPITAEIKGETLESITKIVAESPLNVQDKTDIVKGNGEAI
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                                                                                                                                                                                                                                                       -----NAVVLAVKEVET-------LLTS------IDELAKAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKAN-GTKTKGAE--ELGKLFESV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAGLTKEKDGNTQIDLINEAATAILNNEKEKQANFITLTKNMVNNNALTPDTKVARVNAV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z., Roux V., Raoult D.;
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998 AA;
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109328 MW;
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                                                                                                                                      STAIPEDKQALKDAAS-EAALDRA---TQNFTE
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                                                                                                   ---ILKTNNDKTKGADE--LEKLFESVK
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(Rel. 25, Created) (Rel. 25, Last seq

sequence

STANDARD;

PRT;

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RESULT 11

MYS_AEQIR

ID MYS_A

AC P2473

DT 01-MA

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Best Local S
Matches 91
MYS_AEQIR
P24733;
01-MAR-1992 ()
01-MAR-1992 ()
20-AUG-2001 ()
MYOSIN HEAVY
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                                                                                                                                                    1069
                                                                                                                                                                                                               1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galinski M.R., Medina C.C., Ingravallo P., Barnwell J. "A reticulocyte-binding protein complex of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92315338; PubMed=1617731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, RETICULOCYTE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN RETICULOCYTE CELLS.
SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INVOLVED
                                                                                                                                                  EVNENTEMNTIESSAKEIEALYNELKNKKTSLNEIYQTSNEVK
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                                                                                                                                                                                                             VQDVLTLNEHFNTKQVSNHEPTNFDKSNKSSEELTKAVTDSKTIISK---
                                                                                                                                                                                                                                         ISNLIT - - KKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAIL
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                                                                                                                                                                                                                                                                                                     SIDELAK-----AIGKKIKNDVSLDNEADHNGSLISGAYL------
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Similarity 22.6%;
91; Conservative 5
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1251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
(Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 40, Last annotation updat
Y CHAIN, STRIATED MUSCLE.
                                                                                                                                                                              NDKTKGADELEKLFESVKNLSKAAKEM--LTNSVK
                                                                            STANDARD;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nyitray L., Goodwin E.B., Szent-Gyoergyi A.G.; "Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation.";
                                                                         pfam; pF00063; myosin_head; 1.
pfam; pF01575; myosin_tall; 1.
pRINTS; PR00193; mYOSINLBAVY.
proDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structure 4:21-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF MEDLINE-94173332; PubMed-8127365; Xie X., Harrison D.H., Schlichting I., Sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Alkylation; Calmodulin-binding; 3D-structure.
                                            SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                EMBL; X55714; CAA39247.1;
PIR; S13557; S13557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nyitray L., Goodwin E.B., Szent-Gyorgyi i
"Nucleotide sequence of full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Adductor muscle; MEDLINE-91088319; PubMed-2263488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Adductor muscle; MEDLINE-92011595; PubMed-1917970;
                               PROSITE; PS50096; IQ;
                                                                                                                                                                     InterPro;
                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of the regulatory domain of s resolution: implications for regulation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houdusse A., Cohen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96419133; PubMed=8805510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:306-312(1994).
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                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of the regulatory domain of scallop myosin at
                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MUSCLE CONTRACTION.

FUNCTION: MUSCLE WOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HA

ACTIVITY THAT IS A CTIVATED BY F-ACTIN.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSI

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNIT

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                      1WDC;
                                                                                                                                                                                                                                                     A40997; A40997
                                                                                                                                  Pro: IPR000048; IQ.
pro; IPR002928; Myosin_tail.
pro; IPR00202017; Spectrin.
pro; IPR001009; myosin_head.
PF00612; IQ: 1.
                                                                                                                                                                                                                                   1SCM;
                                                                                                                                                                                                                      30-APR-94.
11-JUL-96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of scallop myosin
tion.";
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WA for a
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                                                                                                                                            STRAIN-X2180-1A;
STRAIN-X2180-1A;
MEDLINE-91185402; PubMed=2010462;
Hirata A., Ogawa Y.,
 Hostetter M.K., Herman D.J., Kendrick K.E.;
                                            SEQUENCE OF 782-1790 FROM N.A
                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
USO1 OR INT1 OR YDL058W.
                                                                                            "A cytoskeleton-related gene, usol, protein transport in Saccharomyces
                                                                                                                                    Nakajima H., Hirata A.,
Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    YEAST
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=4932;
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01-MAY-1992
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                                                                                 Cell Biol.
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                                                                             transport in Saccharomyc
Biol. 113:245-260(1991).
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                         Bendel C.M.,
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Pred. No. 1.
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COLLED COIL (POTENTIAL).
ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY)
ALKYLATION (SH-2) (BY SIMILARITY)
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EMBL; L03188; AAB00143.1;
EMBL; U53668; AAB66659.1;
PIR; A38455; A38455.
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SNAVVLAVKEV---
                                                                                                                                        ADAKEAILK--
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rPro; IPR002017;
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modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPETIBE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
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CHARGED (HYPER-HYDROPHILIC).

DISPENSABLE FOR THE PROTEIN FOR ASP/GLU-RICH (ACTIIC).

G -> E (IN REF. 2).

E -> K (IN REF. 2).

V -> I (IN REF. 2).

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RESULT 13
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                                                  "X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9-A resolution. Biochemistry 35:5404-5417(1996).
                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE-95345067; PubMed-7619796;
                                                                                                                                                                                                                                                                                                           "X-ray structures of the myosin motor discoldeum complexed with MgADP. BeFx abjochemistry 34:8960-8972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762 MEDLINE-95345066; PubMed-7619795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wagle G., Noegel A., Scheel J., Gerisch G "Phosphorylation of threonine residues on Dictyostelium myosin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylatable heavy chain fragment of Dictyostelium myosin FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90353583; PubMed=2387408; Lueck-Vielmeter D., Schleicher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Warrick H.M., de Lozanne A., Leinwand L.A., 9 "Conserved protein domains in a myosin heavy Dictyostelium discoideum.";
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X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) MEDLINE-97452580; PubMed-9305951;
                                                                                                                    x-ray CrysTallography (1.9 angsTroms)
MEDLINE-96206189; PubMed-8611530;
                                                                                                                                                                                                         "X-ray structure of the magnesium(II)-pyrophosphate c
truncated head of Dictyostelium discoideum myosin to
                                                                                                                                                                                                                                            Smith C.
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Last annotation 
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and MgADP.AlF4-.";
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                                                                  1.9-A resolution.",
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to 2.7-A
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                                                                                                                                    Myosin;
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of Mg.2'(3')-O-(N-methylanthraniloy1) nucleotides bound to the blocktyostelium discoldeum myosin motor domain.";
J. Mol. Biol. 274.394.407(1997).
-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ACTIVITY THAT IS ACTIVATED BY ACTIN.
-i- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-AS:
INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MIC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gulick A.M., Bauer C.B., Thoden J.B., Rayment "X-ray structures of the MgADP, MgATPgammaS, of the Dictyostelium discoideum myosin motor Biochemistry 36:11619-11628(1997).
use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. between the Swiss Institute of Bio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN BE SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                               ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE ACTIN-ACTIVATED ATPASE ACTIVITY.
MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN. THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES
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                                                                                                                                                                                          you. It is produced through a collaboration Bioinformatics and the EMBL outstation titute. There are no restrictions of the collaboration of the collaborati
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EMBL; M14628; AAA33227.1; PIR; A26655; A26655.
PIR; A26655; A26655.
PIR; A26655; A26655.
PIR; A26655; A26655.
PIR; B002260; S002260.
PDB; IMMA; 03-DEC-97.
PDB; IMMM; 03-DEC-97.
PDB; IMMN; 17-AUG-96.
PDB; ILVM; 28-JAN-98.
PDB; ILVM; 28-JAN-9

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P49454; Q13246; Q13171;

O1-FEB-1996 (Rel. 33, Created)

O1-FEB-1996 (Rel. 33, Last sequence upd

OT 20-AUG-2001 (Rel. 40, Last annotation u

CENP-F KINETOCHORE PROTEIN (CENTROWERE
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Homo sapiens (Human).
'`arvota; Metazoa; Chordata;
'`arvota; Primates;
             MEDLINE-95379848; PubMed-7651420; Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B., Jones D., Yang-Feng T.L., Lee W.-H.; "Characterization of a novel 350-kilodalton nuclear phosphoprotein
                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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 specifically involved
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kfein R.J., Mack G., Rattner J.B., Yen
protein of the nuclear matrix that ass
at late G2 and is rapidly degraded aft
130:507-518(1995).
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PHOSPHORYLATION (BY MI
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Pred. No. 2.
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Catarrhini; Hominidae
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mitotic-phase progression
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MHCK).
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CHARACTERIZATION.

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CHARACTERIZATION of the kinetochore binding domain of CEN interactions with the kinetochore proteins CENP-F and hBUB J. Cell Biol. 143:49-63(1998)

-:-FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION,

-:-FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION,
                       CONFLICT
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                                                                                                                                                                                                                                  Mitosis;
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                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITINE-95370296; PubMed=7642639; Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.; The C terminus of mitosin is essential for its nuclear localization, centromere/Kinetochore targeting, and dimerization."; J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                               DOMAIN
DOMAIN
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EMBL; U30872; AAA82935.1; -.
EMBL; U25725; AAA86889.1; -.
HSSP; P02649; 1LE4.
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Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., J.
"A novel cell-cycle-dependent 350-kDa nuclear protein:
domain sufficient for nuclear localization.";
Biochem. Biophys. Res. Commun. 212:220-228(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETINOBLASTOMA PROTEIN (RB), C
SUBUNIT: HOMO- OR HETERODIMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBR1.
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                                                                                                                                                                                                                                                           Phosphorylation;
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Query Match Best Local Similarity

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21-JUL-1986 (Rel. 01, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
WOOSIN HEAVY CHAIN B (MHC B).
UNC-54 OR MYO-4.
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MEDLINE-83273600; PubMed-6576334;
Karn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans "protein structural domains in the Caenorhabditis elegans myosin heavy chain gene are not separated by introns.";
myosin heavy chain gene are not separated by introns.";
myosin heavy chain gene are not separated by introns.";
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                     <del>:</del> :
                                                                                                                                                                            SEQUENCE OF 1876-1966 FROM N.A. MEDLINE-83232892; PubMed-6571695; Wills N., Gesteland R.F., Karn J.,
                                                                                                                                                                                                                                             "Periodic charge distributions match cross-bridge spacings in Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2524
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                                                                                                                                                                                                                                                                                           McLachlan A.D., Karn J.
                                                                                                                                                                                                                                                                                                          MEDLINE-82272395;
                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 850-1966 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                  nonsense mutations via altered transfer
                                                                                                                                               "The genes sup-7 X and sup-5 III of C.
                                                                                                                                                                  Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352
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FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                 33:575-583(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKV--QMKEKSSTAMEMLQTQLKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLKAKIEGMTQSLRGLELDVVTIRSEKEDLTNELQKEQERISELEIINSSFENILQEKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEVEALLSSIDEIAAKAIG---KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKAIGKKIKNDVSLDNEADHNGSLISGAYLISNL-----ITKKISAIKDSGELKAEIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                            PubMed=7202124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nematoda; Chromadorea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis.
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er RNA.";
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VVLAVKEVETLLTSIDELAKAIGKKIKN---

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186

VVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKK-----ITESNA LAAE----LDGAQRDLRNTSTDLFKAKNAQE--ELAEVVEGLRRENKS-LSQEIKDLTDQ

·GEGG----RSVHEMQKIIRRLEIEKEELQHALDEAEAALEAEESK

1569

---- DVSLDNEADHNGSLISGAYL

1625

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1415

ALDAANSKNASLEKTKSRLVGDLDDAQVDVERANGVASALEKKQKGFDKIIDEWRKKTDD GLDTENNHNGSL-LAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTD

LGKEGYTDADAKEAILKANGT---KTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP

1527

185

232

1474

128

70

1358

16 SADESVKGPNLTEINKKITDSNAVLLAVK---EVEALLSSIDEI--AAKAIGKKIHQ-NN

SLEEEIEGKN--EILRQLSKANADIQQWKARFEGEGLLKA-DELEDAKRRQAQKINELQE 1414

Query Match Best Local

Local Similarity 23. les 90; Conservative

8.5%;

Score 157.5;

DB 1;

69; Pred.

ed. No. 4; Mismatches

147;

Indels Length 1966;

85;

Gaps

18;

69

В

1570

VLRAQVEVSQIRSEIEKRIQEKEEEFENTRKNHARALESMQASLETEAKGKAELLR----

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                                    MOD_RES
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SMO042; MYSC; 1.
SMART; SMosin; Muscle protein; Coiled coil; Thick filament; Ac
Myosin; Muscle protein; Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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SEQUENCE
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HSSP; P08799; 1MND.
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PYM: TWO CYSTBINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAN SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEGANS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin_tail myosin_head
225125 MW;
                                METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYOSIN HEAD-LIKE
COILED COIL (POT)
                                                                                                                                                                                                                                                                                                                                                                                            HINGE
                                                                                                                                                                                                                                                                                                            LIGHT MEROMYOSIN (LMM) ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA-HELICAL
                                                                                                                                                                                                                                    ACTIN-BINDING
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        CRC64;
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Result
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2 \$70286 outer 2 \$70288 outer 3 \$70285 outer 2 \$69925 outer 2 \$69926 outer 2 \$69926 outer 2 \$69927 outer 2 \$69920 outer 2 \$140287 outer 2 \$69920 outer 2 \$140287 outer 3 \$69920 outer 5 \$69920 outer 5 \$69920 outer 5 \$69920 outer	33.2	33.3	33.5	33.5	33.7	33.7	33.8	33.9	33.9	33.9	33.9	34.2	34.2	34.3	34.5	34.7
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outer s	S70259	140272	S69920	S69926	S69921	S69923	S69925	S70285	I40285	140281	S20543	140108	S70288	S70289	S70286	916695
	outer surface	٠,												outer surface	outer surface	outer surface

Lyme disease spirochete surface protein C	irochete	sease sp		C; Superfamily:	C;	
				Genetics:	→ (:	
	Ip2	strain	source:	A;Experimental source: strain Ip2		
58715; PIDN:AAB36995.1; PID:g1695212	7; NID:98	BL:L4288	nces: EM	A; Cross-references: EMBL: L42887; NID: 9858715;	Α;	
		∀	-210 <li< td=""><td>A; Residues: 19-210 <liv></liv></td><td>A :</td><td></td></li<>	A; Residues: 19-210 <liv></liv>	A :	
	פ ווסר אווס	seduent	e: DNA	A; Molecule type: DNA A:Molecule type: DNA	× 1	
	o not show	200000	70281	A; Accession: S70281	~ ~	
18	ID:962964	0255; MC	mber: S7	Reference nu	Α;	
ind recombination in OspC variation in Lyme di	transfer	lateral	nce for	Title: Evide	Α;	
	995	7-269, 1	. 18, 25	1. Microbiol	MO	
R:Livev I: Gibbs C.P.: Schuster R: Donner F:	ster, R.;	P.; Schu	ibbs, C.	Livey, I.; G	7.	
1301: BIDN:CARA0306 1: BID:G311303	S. NID. C3	> >	210 <jau< td=""><td>A; Residues: 1-210 <jau></jau></td><td></td><td></td></jau<>	A; Residues: 1-210 <jau></jau>		
			e: DNA	A; Molecule type: DNA	۸;	
			iminary	A;Status: preliminary	Α:	
	TD: 93266T	//20; MC	37736	A:Accession: S37726	> A	
es coding for the outer surface protein C (Os	of the gen	ogenity	ic heter	A; Title: Genetic heterogenity of the genes	Α;	
	37-50, 19	1. 182,	. Immuno	d. Microbiol	Me	
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, E.	; Motz, M	uchs, R.	e, S.; F	Jauris-Heipk	æ Þ	
00. 5750.53500467 1. 575.6760604	110 - 101	V	210 KES	A; Residues: 1-210 < RES>	· A:	
			type: DNA	A; Molecule typ	Α;	
from GB/EMBL/DDBJ	ted from (transla	iminary;	A; Status: preliminary; translated	A	
ì		, ,	40269	A:Accession: I40269	A :	
oguence analysis of Bollella pargaoifett sensa	TD-960251	טאפי אוו	mber IA	Peference nu		
Ť.	420, 1995	, 2415-2	DIOI. 33	Clin. Micro	- C	
R; Fukunaga, M.; Hamase, A.	1005		; Hamase	Fukunaga, M.	. 20	
	B31	strain	source:	A; Experimental source: strain B31	Α;	
A;Cross-references: GB:AE000792; NID:g3253098; PIDN:AAC66329.1; PID:g2689901; TIGR:BB	2; NID:93	:AE00079	nces: GB	Cross-refere	Α;	
		v	210 <kle< td=""><td>A; Residues: 1-210 <kle></kle></td><td>Α:</td><td></td></kle<>	A; Residues: 1-210 <kle></kle>	Α:	
		1	e: DNA	Molecule typ	A :	
A:Status: nucleic acid sequence not shown; translation not shown	e not sho	sequenc	eic acid	Status: nucl	Α:	
A:Accessince number: A/OIOO; MOID:30003943	TD: 900009	OTOO; MC	70218	Accession: G	> >	
ase spirochaete, Borrelia burgdorferi.	Lyme dis	nce of a	ic seque	Title: Genom		
	, J.C.	; Venter	th, H.O.	Authors: Smi	Α;	
		997	0-586, 1	ture 390, 58	Na	
	11. C.; C	S.: Fut	Garland,	Bowman, C.:	"	
; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh	uang, W.M	s, S.; H	; Casjen	Fraser, C.M.	R;	
	37726; 57	40269; S	70218; I	Accession: G	<u>ر</u>	
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000	revision	equence_	-1998 #s	Date: 13-Feb	Ü.	
sease spirochete)	i (Lyme d	radorfer	relia bu	Species: Bor	0	
oirochete	Lyme disease spirochete		protein	G70218 Outer surface protein C	 	
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A; Reference number: S72669
A; Accession: S72669
A; Molecule type: DNA
A; Residues: 1-124,'D',126-139,'E',141-210 <JAW>
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Best Local Similarity
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                                                                                                         121
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                                                                                                                                                           1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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                                                          ELTSPVVAESPKKP 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGABELGKLFESVEVLSKAAKEMLANSVK 180
                                                                         ELTSPVVAESPKKP 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                protein C precursor - Lyme disease spirochete (strain PKa)
rrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                Conservative
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97.9%;
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                                                                                                                                                                                                   Score 938; DB 2;
Pred. No. 8.5e-37;
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 945; DB 2
Pred. No. 4e-37;
3; Mismatches
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Query Match
Best Local Similarity 98.3
Matches 174; Conservative
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A;Gene: ospC
C;Superfamily:
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A;Title: Evolution of the Borrelia burgdorferi outer surface prote A;Reference number: I40104; MUID:95286481
A;Accession: I40129
                                                                                             A; Molecule type: DNA
A; Residues: 1-177 <RI
                                                                                                                                                                                                                                   outer surface protein C - Lyme disease spirochete (strain TXGW) (fragment) (Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-200/
                                                                          A; Cross-references:
                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDB.
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                                                         Genetics:
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C)Superfamily: Lyme disease spirochete surface protein
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R;Stevenson, B.; Harthold, S.W.
REMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer surface pr
A;Reference number: I40143; MUID:95154673
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 19-210 <LTV>
A;Cross-references: EMBL:L42893; NID:g858721; PIDN:AAB37001.1;
A;Experimental source: strain 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U04281; NID:9434663; PIDN:AAC43297.1; PID:9434664 F;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: nucleic acid sequence not shown
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 GEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELT
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                 Lyme
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disease spirochete surface protein
                                                                      EMBL: X84783;
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99.4%;
                                                       NID: 9793825; PIDN: CAA59254.1;
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Pred. No. 4.3e-34;
0; Mismatches 1
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                                                                                                                                                                   surface protein OspC
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                                                     PID:9793826
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45.98; 98.38;

Score 853; Pred. No. 5.

DB 2; ..5e-33;

Length 177;

0;

Gaps

0

Mismatches

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outer surface protein C - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_char
C;Accession: S70279
R;Livey, I, Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in C
A;Reference number: S70255; MUID:96296448
A;Accession: S70279
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-193 <LIV>
A;Cross-references: EMBL:L42898; NID:9858729; PIDN:AAB37007.1
A;Experimental source: strain 25015
C;GenetLcs:
A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein C
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A; Residues: 1-211 <RES>
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EMS Microbiol. Lett. 124, 367-372, 1994
Itle: Expression and sequence of outer surface protein eference number: I40143; MUID:95154673
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Matches 158; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFT 119
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                                                                                                                                                                                                                                                                                                                                         KELTSPVVAESPKKP 211
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81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 774.5; DB 2
Pred. No. 2.7e-29;
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                                                                     PIDN: AAB37007.1;
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                                                                     PID:g1695223
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A; Experimental s
C; Genetics:
A; Gene: ospC
C; Superfamily: I
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A; Molecule type: DNA
A; Residues: 1-193 <LIV>
A; Cross-references: EMBL:L42895; NID:g858723;
A: Freerimental source: strain 28354
outer surface protein C precursor - Lyme disease spirochete (strain PBre) C;Species: Borrelia burgdorferi (Lyme disease spirochete) A;Variety: strain PBre A;Variety: strain PBre C;Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000 C;Accession: S69918; S72674; I40103 C;Accession: S69918; S69918;
                                                                                                                                                               RESULT
S69918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination A;Reference number: S70255; MUID:96296448
A;Accession: S70287
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S70287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFTNK 121
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75.1%;
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81.9%;
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Pred. No. 5.9e-26;
7; Mismatches 3(
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Pred. No. 2.
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C;Superfamily: Lyme disease spirochete surface protein C
                                                                                                                                                                                                                                                                         R:Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A:Title: Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu A:Reference number: 140269; MUID:96025162
A:Accession: 140277
A:Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                   Outer surface protein C precursor - Borrelia afzelii
C:Species: Borrelia afzelii
te: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 26-May-2000
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Best Local S
Matches 146
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A; Accession: S72674
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A.Fitle: Molecular analysis of genes encoding outer surface protein C (OspC)
A.Reference number: 140047; MUID:95395018
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A;Residues: 1-152,'E',154-211
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A; Residues: 1-211 < JAU>
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Best Local Similarity 77.6
Matches 152; Conservative
         119 TNKLKEKHTDLGKEGVTDADAKEATLKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
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|perfamily: Lyme disease spirochete surface protein
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                                                                                            AIGQKI-QNNGLAAEADKNGSLLAGAYAISTLIKQKLDGLKGLEGLNKEIAEAKKCSEAF 135
                                                        AIGKKIHONNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETF 118
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                                                                                                                                                                    Similarity 74.5
                                                                                                                                                            37.3%; Score 692.5; DB 2; 74.5%; Pred. No. 1.5e-25; tive 20; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.4%; Score 695.5; DB 277.6%; Pred. No. 1.1e-25
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22; NID:9872021; PIDN:CAA57242.1; PID:9872022
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A;Gene: ospC
C;Superfamily:
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A; Residues: 1-211 <R
                                                                                                                                                                                                                                                                                                                        A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                             Outer surface protein C precursor - Lyme disease spirochete C; Species: Borrella burgdorferi (Lyme disease spirochete) C; Accession: I40268 #sequence_revision 12-Aug-1996 #text_change R; Margolis, N; Hogan, D.; Cieplak, W. Gene 143, 105-110, 1994 A; Title: Homology between Borrelia burgdorferi OspC and members A; Reference number: I40268; MUID:94259285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
I40268
                                                        Query Match
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C:Superfamily: Lyme disease spirochete surface protein
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A;Experimental source: strain ZS7
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A; Residues: 1-193 <LIV>
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Best Local Similarity 77.8%;
Matches 151; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 LKEKHTDLGKEGVTDADAKEAILKANGT-KTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                                                                                                                                                                                                                        <RES>
36.9%; Score 686.5; 73.8%; Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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Pred. No. 1.7e-25;
l0; Mismatches 30
                            DB 2;
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PID: 91041108

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C;Species: Borrelia afzelii
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997
C;Accession: 140273
R;Fukunaga, M, ; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence and A;Reference number: 140269; MUID:96025162
A;Accession: 140273
A;Status: preliminary; translated from GB/EMBL/DDE A;Molecule type: DNA
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A:Molecule type: DNA
A;Residues: 1-190 <LIV>
A;Cross-references: EMBL:L42870; NID:g858737;
A;Experimental source: strain VSDA
C;Genetics:
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C:Superfamily: Lyme disease spirochete surface
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A;Title: Evidence for lateral transfer and record; R:Reference number: S70255; MUID:96296448
A;Accession: S70273
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Best Local Similarity
Matches 146; Conser
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                                                                                                                                                                                                                                                                                                                                                       KKIHQNNGLDTLSNQNGSLLAGAYAISTLITKKLDGLKGSEGLKAEIAEAKKCSEDFTKK 117
                                                                                                                                                                                                                                                                                                                                                                        KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFTNK 121
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                    from GB/EMBL/DDBJ
                                                                                                                                                       Borrelia afzelii
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A;Gene: ospC
C;Superfamily:
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                                                 RESULT
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A;Cross-references: GB:D49379; NID:g1041107; PIDN:BAA08377.1;
C;Superfamily: Lyme disease spirochete surface protein C
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                                                                                                                           182 LTSPVVAESPKKP
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                                                                                                           LTSPVVAESPKKP
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Pred. No. 3.5e-25;
9; Mismatches 26;
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Pred. No. 3.2e-25;
1; Mismatches 26;
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Search completed: March 18, 2002, 09:56:47 Job time: 370 sec
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R;Fung, B.P.; McHugh, G.L.; Leong, J.M.; Steere, A.C.
Infect. Inmun. 62, 3213-3221, 1994
A;Title: Humoral immune response to outer surface protein C of Borrelia burgdorferi in A;Reference number: I40153; MUID:94314437
A;Accession: I4015
A;A
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A:Gene: ospC
C:Superfamily: Lyme disease spirochete surface protein C
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Copyright (c) 1993 - 2000
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Q9R7B2
Q9S3P2
Q44719
Q44999
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EMBL; L42887; AAB36995.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96296448; PubMed=8709845;
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"Evidence for lateral transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyme disease Borrelia."
   123 KEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 182
                                                            61 KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL
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                                                                                                                                                                      KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL
                                                                                                                                                                                                                                                                                            190;
                                                                                                                                                                                                                                                                                                                    Similarity
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192 AA;
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AB36995.1; -.
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20287 MW;
                                                                                                                                                                                                                                                                                                                 50.7%;
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Spirochaetaceae; Borr
                                                                                                                                                                                                                                                                                         Score 943; DB 2;
Pred. No. 2.2e-36;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Query Match
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                                                           MEDLINE=97478003; PubMed=9336916;
Ras N.M., Postic D., Foretz M., Barar
"Borrelia burgdorferi sensu stricto,
U.S.A.'?";
                                                                                                                                                                                                                                Q9R7B1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                 Borrelia burgdorferi (Lyme disease spirochete)
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                      STRAIN-TETS
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=139;
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STRAIN=2-1498 CA4;

Probert W.S., Crawford M.R., Cadiz R.B., LeFebvre R.B.;

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; L81131; AAB06569.1; -.

InterPro; IPR001800; Lipoprotein_6.

Pfam; PP01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
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NCBI_TaxID=139;
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01-FEB-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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                              Syst. Bacteriol. 47:1112-1117(1997)
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Pred. No. 1.2e-35;
                                                                                         Baranton G.;
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                                                                     a bacterial
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01-MAY-2000
01-MAY-2000
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Genetics 151:15-30(1999).
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99091544; PubMed=9872945; Wang I.N., Dykhuizen D.E., Qiu W., Dunn J.J., Bos Genetic diversity of ospC in a local population
                                                                                                                                                                                                                                                                                                                                       EMBL; AF029860; AAB86543.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi (Lyme Bacteria; Spirochaetales;
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U91798; AAB81895.1;
InterPro; IrR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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DE PROTEIN C (FRAGMENT).
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DE OUTER SURFACE PROTEIN C (FRAGMENT).
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OS Borrella burgdorferl (Lyme disease spirochete).
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(TremBLrel. 13, Last sequence update)
(TremBLrel. 17, Last annotation update)
DE PROTEIN C PRECURSOR (FRAGMENT).
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21307 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 893; DB 2;
Pred. No. 4.4e-34;
3; Mismatches 1
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ring heterogeneous
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181 VA J
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01-JAN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
OUTER SURFACE PROTEIN C
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                                    InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1.
                                                       Wang I.-N., Dykhuizen D.E.,
Submitted (OCT-1997) to the
EMBL; AF029869; AAB86552.1;
                                                                                                                         Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marti-Ras N., Postic D.,
Submitted (MAR-1997) to tl
EMBL; U91797; AAB81894.1;
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                                                                                      STRAIN-OC10;
                                                                                              SEQUENCE FROM N.A.
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Pfam; PF01441; Lipoprotein_6; 1.
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                              ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 98.9
80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F01441; Lipoprotein_6; 1.
PD001149; Lipoprotein_6; 1.
                           PD001149; Lipoprotein_6; 1.
191
191
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(TremBLrel. 05, Last sequence update)
(TremBLrel. 17, Last annotation updat
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182 AA;
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19202 MW;
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20502
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i sensu stricto, a bacterial
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to the EMBL/GenBank/DDBJ
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                                                                                                                        spirochaetaceae;
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1; Mismatches
                                                                 Dunn J.J., Luft B
EMBL/GenBank/DDBJ
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 E4FB56BCB61740F9
                                                                                                                                  spirochete)
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Query Match 47.6%; Best Local Similarity 100.0%; Matches 181; Conservative

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Score 885; DB 2; Pred. No. 9.6e-34;); Mismatches 0;

Length 191;

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Gaps

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 Q44719
Q44719;
01-NOV-1996
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Livey I., Gibbs C.P., Schuster R., Dor
"Evidence for lateral "transfer and rec
Lyme disease Borrelia";
Mol. Microbiol. 18:257-269(1995).
EMBL; L42893; AAB37001.1.;
InterPro; IPRO01800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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NON_TER
SEQUENCE
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Q9S3P2;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
Q1-JUN-2001
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P2
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                                                                                                                    Bacteria; Spirochaetales; Spirochaetaceae; Borr
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                              Local 180;
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(TrEMBLrel. 01, Created)
                                                                                                                                                                                   192
192 AA;
              PRELIMINARY;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                              192
20472 MW; 46AC8F93E4DFED6C CRC64;
                                                                                                                                                       47.38;
99.48;
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                                                                                                                                              Score 879; DB 2;
Pred. No. 1.8e-33;
0; Mismatches 1
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                                                                                                                                                                                                                                         recombination
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            AA
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T "Expression and sequence of outer surface protein C among N "Marthold Stevenson B., Barthold Stevenson B., Barthold Stevenson Boundary Down Pfolm; Pfold1800; Lipoprotein_6; 1.

DR ProDom; Pfold141; Lipoprotein_6; 1.

DR ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 210 AA; 22526 MW; 2D672991D584E4EE CRC64;
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Best Local
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Q44999;
Q1-NOV-1996;
Q1-NOV-1996;
Q1-JUN-2001;
                   NON_TER
                                                                "Evolution of the Borrelia burgdorferi outer J. Bacteriol. 177:3036-3044(1995).
EMBL; X84783; CAA59254.1;
        SEQUENCE
                                         ProDom;
                                                  Pfam; PF01441;
                                                                                                                                                                                                             U1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                            Hansen K.;
                                                                                                                   Theisen M., Borre
                                                                                                                             MEDLINE=95286481; PubMed=7768799;
                                                                                                                                            STRAIN-TXGW,
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                           Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                             InterPro; IPR001800;
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MEDLINE=95154673; PubMed=7851744;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDELAKAIGKK
                                  o; iPR001800; Lipoprotein_6.
F01441; Lipoprotein_6; 1.
PD001149; Lipoprotein_6; 1.
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Similarity 99.4%;
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       AA;
 177
18800 MW;
                                                                                                              M., Mathiesen M.J., Mikkelsen
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17,
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Spirochaetaceae; Borr
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156671B9614E7A2D CRC64;
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Last annotation update)
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                                                                                      surface protein OspC.";
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                                                                                                              В.,
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                                                                                                             Lebech A.M.,
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RESULT
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Query Match
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Matches 174
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Theisen M., Frederiksen B., Lebech A.M., Vuust J., Ha
"Polymorphism in ospC gene of Borrelia burgdorferi an
immunoreactivity of OspC protein: implications for ta
use of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
EMBL; X73622; CAA52001.1;
InterPro; IPRO1800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
OSPC.
                 O9R7B4 PRELIMINARY; PRT; 175 AA.
09R7B4;
09R7B4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
BOrrelia burgdorferi (Lyme disease spirochete).
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Bacteria;
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ilarity 97.8%;
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No. 6.8e-32;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel
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                                                                                        Marti-Ras N., Postic D., Foretz M., Submitted (MAR-1997) to the EMBL/Ge EMBL; U91801; AAB81898 1.; InterPro; IPRO01800; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6; 1.
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Ras N.M., Postic D., Foretz M., B
"Borrelia burgdorferi sensu stric
                                                                                                                                                                                                                                                                                                     MEDLINE-97478003; PubMed-9336916; Ras N.M., Postic D., Foretz M., Bara "Borrelia burgdorferi sensu stricto,
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to the EMBL/GenBank/DDBJ
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01-NOV-1996
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                                                                                        Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; s
                                                                                                                                                                                             OSPC
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   SEQUENCE FROM N.A
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Lawson C.L., Swaminathan S.;
"Crystal structure of outer surface prote
disease spirochete, Borrelia burgdorferi.
EMBO J. 0:0-0(2001).
EMBL; AF337548; AAK21289.1; -
VARIANT 161 AK21289.1; -
VARIANT 161 AK21
                                                                 NCBI_TaxID=139;
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Bacteria; Spirochaetales; Spirochaetaceae; Borr
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Spirochaetaceae; Borrelia
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Best Local Similarity
Matches 158; Conserv
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"Expression and sequence of outer surface protein C among American isolates of Borrelia burgdorferi.";

FEMS Microbiol. Lett. 124:367-372(1994).

EMBL; U04282; AAC45540.1;

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 211 AA; 22603 MW; 63984BA6D8743ED5 CRC64;
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MEDLINE=95154673; PubMed=7851744;
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Search completed: March 18, 2002, 10:10:53 Job time: 976 sec

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2. /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3. /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

4. /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5. /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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7	Outer surface prot	Borrelia ZS7 antig	B. burgdorferi Osp	B. burgdorferi sen	Borrelia 25015 Osp	Borrelia 25015 ant	Borrelia 297 antig	Borrelia B31 antig	B burgdorferi ospC	rgdorferi	B31 outer surface	urgdor	B31 Osp-A/antigen	feri	Borrelia IP2 OspC	face	rgdorferi	B31 outer surface	qs		qs	Borrelia sp chimer	Borrelia sp chimer		Borrelia sp chimer	qs	gp	qs			Borrelia sp chimer	Borrelia sp chimer	Ö	Borrelia sp chimer	

ALIGNMENTS

Chimeric - Chimeric -03-APR-2001 (first entry) AAB62713; AAB62713 standard; Protein; (UYNY) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC. 18-JUN-1999; 19-JUN-2000; 2000WO-US16915 28-DEC-2000 WO200078966-A1 Borrelia; Borrelia sp chimeric ospC protein SEQ ID NO: ospC; Lyme disease; vaccine; chimeric protein; tick. Borrelia sp. Borrelia sp. 99US-0140042 377 ₽ K

Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease - $\,$

WPI; 2001-050113/06. N-PSDB; AAF29017.

Dattwyler RJ,

Seinost G,

Dykhuizen

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Luft BJ,

Gomes-Solecki M;

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Chimeric -
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                                                                                           Borrelia; ospC; Lyme disease; vaccine; chimeric protein;
                                                          28-DEC-2000
                                                                    WO200078966-A1
                                                                                                         Borrelia sp chimeric
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                                                                                                                                AAB62739;
                                                                                                                                         AAB62739 standard;
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                                                                                                                                                                                                                                                                                                                                                           The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
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Borrelia
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  18-JUN-1999;
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Chimeric -
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Pred. No. 1.1e-122;
7. Mismatches 2;
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Query Match
Best Local S
Matches 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions of OspC |
Lyme disease are used
to Lyme disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                            AAB62712
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)B; AAF29033.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
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(first entry)
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d to immunize
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Pred. No. 1.9e
3; Mismatches
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detect immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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protein

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Chimeric - Chimeric -

Borrelia;

18-JUN-1999;

19-JUN-2000;

Dattwyler RJ,

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121 KLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leaves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 43; Page 83-84; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
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DB; AAF29016.
                      standard;
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                     Protein;
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Pred. No. 1.1e.
20; Mismatches
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Best Local S
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384
               362 LAKAAKEMLANSVKEL 377
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                                        302 KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAABLEKLEKAVEN
                                                                                                                        205
                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                               145
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                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions of OspC polypeptides from strains of Borrelia which Lyme disease are used to immunize animals and detect immune response to Lyme disease -
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Chimeric -
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                             \verb|eiekakkcseeftaklkgehtdlgkegvtddnakkailktnndktkgadeleklfesvkn|
                                                                     LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIE
                                                                                                                                                                | LKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE
                                                                                                              ltspvvaespkkpsmvnnsgkdgntsansadesvkgpnlteiskkitesnavvlavkeve
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                                                                                                                                                                                             326;
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                                                                                                                                                                                                                                                                                             Similarity
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86.7%;
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Pred. No. 7.2
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es 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 43; Page 78-79; 160pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric -
Chimeric -
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                                                                                                                                                                                                                                                                                   disease are used
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Borrelia
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d to immunize animals and o
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Pred. No. 7.1e-104;
2; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PJ,
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N-PSDB;
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Lyme disease are used
to Lyme disease -
                                                                                                                                                                                            The present invention provides compositions comprising ospC protein chimeric ospC proteins from members of the Borrelia genus. These members of the Borrelia genus. These members aparinii. These can be used vaccines against Borrelia infection, which is spread by ticks and
                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric -
Chimeric -
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                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                    to Lyme
                                                                                                                                                                                                                                                                                                           Dattwyler RJ,
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                                                                                                                                                                                    to Lyme disease.
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357 lskaakemltnsvkel 372
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                                                                                                                                      Local Similarity
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         LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIE
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Borrelia
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                                                                                                                              Score 1558; DB 22;
Pred. No. 1.3e-103;
3; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
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Matches 326
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                                                                                                                                                                                                                                                                       Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                                                                                Sequence
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   121 KLKEKHTDLGKEGVTDADAKEAILKANGT-KTKGAEELGKLFESVEVLSKAAKEMLANSV
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                                  GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLK-NEGLKEKIDAAKKCSETFTN 120
                        {\tt gkkikndgsldneanrnesllagaytistlitgklsklngseglkekiaaakkcseefst}
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                                                                                                                      Similarity
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Borrelia
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86.2%; Pred. No. 6.5e-101;
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al Similarity 325; Conserv

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Score 1516.5; DB 2; Pred. No. 1.2e-100; 1; Mismatches 31;

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                           The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
Sequence
                                                                                                                Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                   Claim 43; Page 131;
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Query Match

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Score 1480.5;

В

22;

Length

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leave

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Sequence

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disease.

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leaves the same provided that the same provided in the same provided that the same provided th

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Claim 43;

Page 102-103; 160pp;

English

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                                                   to Lyme
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Best Local S
Matches 309
        Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                              N-PSDB;
                                                                          Dattwyler RJ,
                                                                                              (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                                                                           18-JUN-1999;
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Chimeric -
WPI; 2001-050113/06
              Dattwyler RJ,
                          (UYNY ) UNIV NEW YORK STATE RES FOUND.
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                                                               19-JUN-2000; 2000WO-US16915
                                                                                                                                  Borrelia; ospC; Lyme disease;
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                                                                                                                                                               03-APR-2001
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tive 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 43; Page 112-113; 160pp;
                                                                                                   Borrelia; ospC;
                                                                                                                  Borrelia sp
                                                                                                                                     03-APR-2001
                                                                                                                                                                       AAB62737 standard;
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        18-JUN-1999;
                       19-JUN-2000; 2000WO-US16915
                                                         WO200078966-A1
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Lyme disease are used
to Lyme disease -
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                           KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
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1: /cgn2_6/ptodata/2,

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US-08-235-836C-30
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US-07-903-580-2
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	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appl1	Sequence 2, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 8, Appli

US-08-235-836C-110 US-08-235-836C-110 Sequence 110, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION: TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO: FILING DATE: 29-APR-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/ FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin J. APPLICANT: Luft, Benjamin J. TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising TITLE OF INVENTION: Borrella Polypeptides and Uses Therefor NUMBER OF SEQUENCES: 144 CORRESPONDENCE ADDRESS: NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324 REFERENCE/DOCKET NUMBER: BNL93-28A TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338 SEQUENCE CHARACTERISTICS: LENGTH: 466 amino acid TOPOLOGY: linear MOLECULE TYPE: protein COUNTRY: USA ZIP: 11973 STATE: Upton APPLICATION NUMBER: ADDRESSEE: amino acid PatentIn Release #1.0, Brookhaven National Laboratory us/08/235,836C US 08/148,191 Version #1.25

Query Match 52.6 Best Local Similarity 62.9 Matches 224; Conservative

52.6%; 62.9%;

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Patent No. 5620862
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CAITCLL, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                  TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,353
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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STRANDEDNESS: sir
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETN 120
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                                                                      Conservative
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                                                                                  51.1%;
97.9%;
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Methods for Diagnosing Early Lyme
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                                                                               Score 945; DB 1;
Pred. No. 2.3e-64;
                                                                                                                                                                                                                                                                                                          UCT93-05
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Version
                                                                                             Length 210;
                                                                   Indels
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                                                              Gaps
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Patent No. 6
                                                                                                          DESCRIE: N...
HYPOTHETICAL: N...
HYPOTHETICAL: N/A
                                                                                                                                                                                                                                                     TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                      ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
IMMEDIATE SOURCE:
LIBRARY: DSM 5662
 IDENTIFICATION METHOD: PUBLICATION INFORMATION:
                               FEATURE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
                                           POSITION IN GENOME:
                                                                                                                                                                             TOPOLOGY: LINEAR MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: 3.5" FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                             DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOTZ, MANFRED
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                                           N/A
amino acid analysis
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REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PK
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" FLOPPY DISC COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WILSKE, BETTINA PREAC-MURSIC, VERA
                                                                                                                                                                                                                                                                                                                      MS-DOS Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNOLOGICALLY ACTIVE PROTEINS
                                                                                                                                                                             PCT/EP90/02282
                                                                                                                                       US 07/862,535
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US-08-209-603E-15

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APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: US 08/209/02282
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-06-13
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US-09-196-293-15
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Best Local Simi
Matches 189;
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Best Local Similarity
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                                                                                                                                                                                                                           Matches
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 15
LENGTH: 209
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                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                    121
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                                                                                                                                                                   1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
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                                                                                          IGKKIHONNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
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                                  KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                         IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                                                         188;
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                                                                                                                                                                                                                     Score 933; DB 4;
Pred. No. 1.9e-63;
3; Mismatches 1
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Pred. No. 7.9e-64;
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                                                                                                                                                                                                                                                          Length 209;
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                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION: IMPORMATION:
THE TENDAME: 7516, 282-7738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 ELTSPVVAESPK 208
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                  181 ELTSPVVAESPKKP 194
                                                                                                       121
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STATE: NY
COUNTRY: USA
ZIP: 11973
 197
                                                                    137
                                                                                                                                                         61 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
                                                                                                                                         77
                                                                                                                                                                                                          17 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                              1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                      KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                                                                         IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
                                                                  KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
ELTSPVVAESPKKP
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6248562
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                               50.4%;
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                                                                                                                                                                                                                                                                           Score 932; DB 4;
Pred. No. 2.2e-63;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides and Uses Therefor
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                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                 210;
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RESULT

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TYPE: amino a

TOPOLOGY: lir

MOLECULE TYPE:

US-08-235-836C-122
                                                                                                                 US-08-235-836C-107
                                                                   Sequence 107, Applicat Patent No. 6248562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MARGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPHONE: (516) 282-3729
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: BTIS COLING SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-235-836C-122; Sequence 122, Application US/08235836C; Patent No. 6248562; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   atches 191;
                          TITLE OF INVENTION:
                                            APPLICANT:
                                                                                                                                                                                                184 SPVVAESPKKPSMVNNSGKDGNTSANSADESVK 216
                                                                                                                                                                                                                         APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
RUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/235,836C FILING DATE: 29-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                   SPVVAESPKKPGTMAQYNQMHMLSNKSASQNVR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i: 588 amino acids amino acid
Dunn, John J.
Luft, Benjamin J.
VENTION: No. 6248562el Chimeric Proteins Comprising
                                                                                                 Application US/08235836C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΥN
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                            50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             16;
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US-08-158-353-2
                                                                                      Sequence 2, Application US/08158353
Patent No. 5620862
GENERAL INFORMATION:
APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for Diagnosing Early Lyme
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (516) 282-73:
TELEPAX: (516) 282-3729
INFORMATION FOR SEQ ID NO:
                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                           456 SPVVAESPKKP 466
                                                                                                                                                                                                                                                                                                           184 SPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                  336 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: (FILING DATE: 29-APR-)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COUNTRY:
                      CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGK 335
               STATE:
                                      ADDRESSEE: Hamilton, Brook, Smith & Reynolds, STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   64 KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 NNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLGSIDEIAAKAIGK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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CITY: Upton
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bogosian, Margaret C
REGISTRATION NUMBER: 25,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186;
             M
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amino acid
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Pred. No. 1.3e-61;
1; Mismatches 4; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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US-08-158-353-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                      08-031-295-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE TITLE OF INVENTION: PREVENTION OF LYME DISEASE NUMBER OF SEQUENCE: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Carroll, Alice O.
                                                                                                                                                                                                                                                                                                APPLICANT: LIVEY, Ian APPLICANT: DORNER, Freidrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                        196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 SVKELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 NKLKEKHTDLG--KEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLAN 177
                                                                                                                                                                         ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
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Local Similarity 74.1%;
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TOPOLOGY: 11r
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REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT93-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/158,353 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                               COUNTRY:
            APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKELTSPVVAENPKKP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKLKSSHAELGIANGAATDANAKAAILKTNGTKDKGAQELEKLFESVKNLSKAAQETLNN
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                                                                                                                                               20007-5109
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Pred. No. 1e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 212;
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US-07-903-580-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,580
FILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
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APPLICATION NUMBER: I
FILING DATE: 25-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Ereidrich
TITLE OF INVENTION: METHOD AN
TITLE OF INVENTION: PREVENTIO
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 VKELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07 FILING DATE: 22-JAN-1992
                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
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                                                                                                                                                                                                     CITY: Alexandria
                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MACNNSGKDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKELTSPVVAETPKKP 212
                                                                                                                                                                                                                                                                                                                                                                                                          Application US/07903580
                                                                                                                                                                                   Virginia
                                                                                                                                                                                                                      E: Foley & Lardner
1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.2%;
                                                                                                                                                                                                                                                                                               METHOD AND PREVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us 07/903,580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 670; DB 1;
Pred. No. 1.4e-43;
                                                                                                                                                                                                                      Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                               COMPOSITION FOR OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 212;
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PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 22-JAN APPLICATION NUMBER:

22-JAN-1992

US 07/824,161

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                              08-158-353-4
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SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
                                 ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
                                                                                        SOFTWAKE: FACTOR DATA:
CURRENT APPLICATION DATA:
US/08/158,353
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Padula, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 VKELTSPVVAETPKKP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 TNKLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 VKELTSPVVAESPKKP 194
                                                                                     APPLICATION NUMBER: FILING DATE:
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         REFERENCE/DOCKET NUMBER:
                        REGISTRATION NUMBER:
                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                     CITY: Lexington
                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 36.2%; Score 670; DB 4; Length 21 Local Similarity 73.0%; Pred. No. 1.4e-43; Nes 143; Conservative 15; Mismatches 36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                                                                                                                                       Two Militia Drive
                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                               Padula, Steven J.
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11-JUL-1991
                                                                                                                                                                                                                                                                                                                                  Disease
                                                                                                                                                                                                                                                                                                                                         Methods for Diagnosing Early Lyme
         UCT93-05
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                                                                                                                            Version #1.25
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APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Presc-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT ETLING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO 7/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
                                                                                               ; ORGANISM: Borrelia burgdorfer;
US-09-196-293-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-196-293-11
Query Match
Best Local Similarity
Matches 138; Conserv
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                                                                                                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 137;
                                                                                                                                                                                                                                      EARLIER FILING DATE: 1990-12-21

EARLIER APPLICATION NUMBER: DE P39 42 728.5

EARLIER FILING DATE: 1989-12-22

EARLIER APPLICATION NUMBER: DE P40 18 988.0
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                     EARLIER FILING DATE: 1990-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fuchs, Renate APPLICANT: Motz, Manfred
                                                                                                                                  TYPE: PRT
                                                                                                                                                 ENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 VKELTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 VKELTSPVVAESPKKP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soutscheck, Erwin
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                                                                                                                                                                                  Windows Version 4.0
                 34.0%;
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           Score 629; DB 4;
Pred. No. 1.8e-40;
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                               Length 212
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Conservative

13;

Mismatches

Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: AT&T : IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS VETSION 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,603E
FILING DATE: 10-MAR-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                 TELEFAX: (212) 557-563:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-WURSIC, VERA
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PRO
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: LK TELECOMMUNICATION INFORMATION:
                                            HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
              IMMEDIATE SOURCE:
LIBRARY: DSM 5
                                                                                                                                 MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
NAME: ROBINSON, WILLIAM R.
127,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 VKELTSPVVAESPKKP 194
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STATE: NY
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                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0' FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                    AMINO ACID
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                                                                                                                                                                                                                                                         (212) 557-5635
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              DSM 5662
                                                                                                                                                                                                                                                                           (212)
                                                                                                                                    PROTEIN
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US-08-235-836C-34
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 138;
                                                                                                                               APPLICATION NUMBER: US 08/148
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                               TELEFAX: (516) 282-37
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD: PUBLICATION INFORMATION: ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994 CLASSIFICATION: 435
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                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Brookhaven National Laboratory
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NY
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                                            amino acid
                                                                212 amino acids
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                                  linear
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                                                                                                                    282-3729
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70.4%;
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                                                                                                                                                                                                                                                         US 08/148,191
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;; Pred. No. 1.8e-40;
13; Mismatches 43
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N/A
                                                                                                                                                                    BNL93-28A
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                                                                                                                                                           ; LENGTH: 209 amino acids
; TYPE: maino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-836C-32
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; Sequence 32, Applicat:
; Patent No. 6248562
; GENERAL INFORMATION:
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                                                              Query Match
Best Local Similarity
Matches 133; Conserv
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APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994

CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSÍAN, MAIGARTE C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.8
Best Local Similarity 69.4
Matches 136; Conservative
                                                                                                                                                                                                                                                                      TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
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ZIP: 11973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Upton

    Application US/08235836C
6248562

                                                                 Conservative
                                                          33.2%; Score 614.5; DB 4; 68.2%; Pred. No. 2.2e-39; ative 20; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%; Score 626; DB 4; Length 21 69.4%; Pred. No. 3e-40; tive 16; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 212;
                                                            Indels
                                                                                             Length 209;
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Search completed: March 18, 2002, 09:55:33 Job time: 346 sec

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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                Score
  100.0
100.0
98.6
98.6
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97.1
96.9
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Match
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Gapop 10.0 , Gapext 0.5
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cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MACNNSGKDGNTSANSADES.....AVENLAKAAKEMLANSVKEL 377
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1850
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               US-09-596-746A-30
US-09-596-746A-82
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US-09-596-746A-26
US-09-596-746-62
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168.507 Million cell updates/sec
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S-09-596-746-7	S-09-596-746A-	-09-596-746-38	S-09-596-746A-	-09-596-746-7	-09-596-746-4	-09-596-746A-4	-09-596-746A-	-09-596-746-68	-09-596-746-3	-09-596-746A-	-09-596-746A-6	-09-596-746-6	S-09-596-746-3	S-09-596-746A-3	-09-596-746A-	-09-596-746-7	-09-596-746A-	S-09-596-746-5	-09-596-746-56	S-09-596-746A-	S-09-596-746A-7	S-09-596-746-7	S-09-596-746-4	S-09-596-746A-	-09-596-746A-6	S-09-596-746-6	S-09-596-746-36	-09-596-746A-	S-09-596-746A-6	S-09-596-746-6	S-09-596-746-2	09-596-746A-2	-09-596-746A-	09-596-746-	96-746A-
nce 76, App	nce 38,	nce 38, App	nce 72, App	nce 72,	nce 40,	nce 40,	nce	nce 68,	nce 32,	nce 32,	nce 64, App	nce 64, App	nce 34, App	nce 34, App	nce 78, App	nce 78, App	nce 52, App	nce 52, App	nce 56, App	nce 56, App	nce 74, App	nce 74, App	nce 42, App	e 42, App	1ce 66, App	nce 66, App	1ce 36, App	nce 36, App	nce 60, App	nce 60, App	nce 24, App	nce 24, App	nce 80, App	Sequence 80, Appl	nce 28, App

ALIGNMENTS

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; FEATURE:
; OTHER INFORMATION: OSPC Chimera
US-09-596-746-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-596-746-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
Query Match 100.0%; Score 1850; DB 19; Best Local Similarity 100.0%; Pred. No. 3.4e-125; Matches 377; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                            SOFTWARE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C: Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                             377
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    Indels
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  Gaps
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1 MACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60

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; OTHER INFORMATION: OSPC Chimera US-09-596-746A-30
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US-09-596-746A-30
                                                                                                                                                                                                                                          Query Match
Best Local
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease.
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT APPLICATION NUMBER: US/09/596,746A
PRIOR APPLICATION NUMBER: US/01/40,042
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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181 ELTSPVVABSPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI 240
                                                                                       121
                                                                                                                  61
                                                                                                                                           61
                                                                                                                                                    Local Similarity
mes 377; Conserv
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                                                        KLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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Seinost, Gerald
                                                                                                                                                                                                                    100.0%; ; ilarity 100.0%; ; Conservative 0;
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                                                                                                                                                                                                              Score 1850; DB 19; Length Pred. No. 3.4e-125; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
CURRENT APPLICATION NUMBER: US/09/596,746
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
                                  362 LAKAAKEMLANSVKEL 3.77
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                                                                                                                                                                                                                                                                                                                                                        2 ACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSGIDEIAAKAI
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                    LAKAAKEMLANSVKEL
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Scinost, Gerald.
APPLICANT: Sythizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelli That Cause Lyme Disec
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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US-09-596-746A-26
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: SEQ ID NO 82
: LENGTH: 401
: TYPE: PRT
ORGANISM: OSPC Chimera
J-09-596-746A-82
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Best Local S
Matches 372
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PRIOR FILING DATE: 199-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PARTY.
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
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llarity 98.9%; Pred. No. 2.4e-123;
Conservative 2; Mismatches 2;
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                                                                  Disease in
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; OTHER INFORMATION: OSPC Chimera US-09-596-746-26
                                                                                                                                                                                                                                                                                                                            US-09-596-746-26
                                                                                                                                           APPLICANT: Dattwy...,
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
TITLE OF INVENTION: Borrelia 122111 That Cause Lyme Di
                                                                 SOFTWARE: Fate SEQ ID NO 26 LENGTH: 373
                                                                                                                                                                                                                                                                                               Sequence 26, Applica GENERAL INFORMATION:
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SEQ ID NO 26
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Best Local Similarity
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                          NUMBER OF SEQ ID NOS:
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TYPE: PRT
ORGANISM: Artificial Sequence
                         TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                             FastSEQ for Windows Version 4.0
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98.1%;
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Pred. No. 1.1e-121;
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98.1%;

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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 397
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: ospC Chimera
US-09-596-746-62
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US-09-596-746-62
US-09-596-746-02
US-09-596-746-
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nes 369; Conserv
GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETFTNK 121
                                                                                                    GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK
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Pred. No. 4.4e-121;
3; Mismatches 2;
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LAKAAKEMLANSVKEL

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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 62
; LENGTH: 398
; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANY: Dykhuizen, Danial
APPLICANY: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEG ID NOS: 84
SOFTWARE: FastSEO for Windows Version 4.0
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Best Local S
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APPLICANT:
362 LAKAAKEMLANSVKEL 377
                           323
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hes 368;
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382 LAKAAKEMLANSVKEL
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                  KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
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Seinost, Gerald
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97.98;
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Pred. No. 4.4e
3; Mismatches
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APPLICANT: Dythuizer, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 378
TYPE: PRT
US-09-596-746A-28
; Sequence 28 Application US/09596746A
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Seinost, Gerald
; APPLICANT: Dykhuizen, Danial
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Maria J.C. Gomes-Solecki
; TITLE OF INVENTION: Groups of Borrelia burgdorferi and
; TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
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Best Local S
Matches 331
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APPLICANT: Dattwyler, Raymond J.
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Seinost, Gerald
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hes 25;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Sykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Goroups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Dise:
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
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CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                            Sequence 80, Application US/09596746 GENERAL INFORMATION:
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Best Local Similarity
Matches 331; Conserv
                                                                        NUMBER OF SEQ ID NO
SOFTWARE: FastSEQ
SEQ ID NO 80
ORGANISM: OSPC Chimera
-09-596-746-80
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ORGANISM: Artificial Sequence
FEATURE:
                                       TYPE: PRT
                                                           LENGTH:
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                                                                                            NOS: 84
EQ for Windows Version
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US-09-596-746A-80
Sequence 80, Application US/09596746A
GENERAL INFORMATION:
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Best Local S
Matches 326
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APPLICANT:
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APPLICANT: Luft, Benjamin J
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEO ID NOS: 84
                                                                                                                                                                                                                                                       LENGTH: 402
TYPE: PRT
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         122 LKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE
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                                                                                                                                                  / Match 85.9%; Score 1589.5; DB 19; Length 402; Local Similarity 86.7%; Pred. No. 2.5e-106; Local Similarity 22; Mismatches 27; Indels 1;
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                                                    GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETNK 121
                                                                                          GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 145
 2 ACNNSGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDETAAKAI 61
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LENGTH: 375
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/09/596,746A

CURRENT FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

SOFTWARE: F8stSEQ for Windows Version 4.0
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       297
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                       EKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVE
                                                    ETLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK
                                                                     ETLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLK
                                                                                                                            ELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI 240
                                                                                                              ELTSPVVAES---PAMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEV
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hes 27;
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APPLICANT: Seinost, Geraid
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEO ID NOS: 84
NUMBER OF SEO ID NOS: 84
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US-09-596-746-60
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Sequence 60, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
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LENGTH: 374
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Best Local Similarity 85.9%;
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ORGANISM: Artificial Sequence
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                                                                                                                                         LAKAAKEMLANSVKEL 377
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| LSKAAKEMLTNSVKEL 372
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                                                                                                                                                                                                       EIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKN
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; Pred. No. 2.6e-104;
22; Mismatches 27;
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; ORGANISM: OSPC
US-09-596-746-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR TILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 398
TWOTE: DDT
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Best Local Similarity
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                                                                                                                                                   242 TLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKE 301
                                                                                                                                                                                                                    182 LTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIE 241
                                                                                                                                                                                                                                                                   302 KIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
                                                                                                                                  262 TLLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKA
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LSKAAKEMLTNSVKEL
                                                                   GKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
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Maria J.C. Gomes-Solecki
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Search completed: March Job time: 972 sec 18, 2002, 10:08:44

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*
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Match
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Gapop 10.0 ,
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                    US-09-974-992-5

US-09-974-992-7

US-09-9708-427-19882

US-09-708-427-19881

US-09-708-427-19881

US-09-742-096-5

US-09-742-096-3

US-09-742-096-3

US-09-708-427-3729

US-09-708-427-3729

US-09-708-427-3729

US-09-708-427-32622

US-09-708-427-32623

US-09-708-427-32623

US-09-708-427-32623

US-09-708-427-3263

US-09-708-427-3263

US-09-815-242-5834

US-09-815-242-5839

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Sequence
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19883, A
19881, A
15521, A
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SAN	Lon US/0997 Marianne Michael Ine, Soren Novel OspC 1666p 2001-10- 1999-05-13 MBER: PCT/ 1999-05-02 37.4%; 37.4%; 37.4%;	2434 2434 837 837 875 730 1313 3070 31070 7138 763 763 1304 1490 11890 11890 11890 11890 11890 11890 11890 11890 11890 11890
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2; Mismatches 30; 2; Mismatches 30; 2; PNLTEINKKITDSNAVLLAVK	4992 J. derived peptide fragm /09/974,992 10 80,089 DK97/00203	US-09-815-242-5835 US-10-072-851-883 US-10-072-851-5883 US-10-072-851-5883 US-09-815-242-13080 US-10-072-851-13080 US-09-708-427-15044 US-09-708-427-15044 US-09-708-427-21267 US-09-708-427-21266 US-09-708-427-15045 US-09-614-150-10224 US-09-614-150-10311
Indels 3; Gaps EVEALLSSIDEIAAKA 60	ents	Sequence 5835, Ap Sequence 5835, Ap Sequence 5883, Ap Sequence 13080, A Sequence 13080, A Sequence 15044, A Sequence 7, Appli Sequence 7, Appli Sequence 21265, A Sequence 10245, A Sequence 10245, A Sequence 10214, A Sequence 10311, A Sequence 6536, Ap Sequence 6536, Ap Sequence 6536, Ap Sequence 17, Appli Sequence 17, Appli Sequence 10, Appli
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RESULT 2 US-09-974-992-7

Sequence 7, Application US/09974992 GENERAL INFORMATION:

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APPLICANT: OSTERNATION: NOVEL OSPC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 207
TYPE: PRT
                                                                                                              ; ORGANISM: Borrelia
US-09-974-992-3
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           Query Match 32.2
Best Local Similarity 66.0
Matches 128; Conservative
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APPLICANT: Theisen, Michael
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel Ospc-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT APPLICATION NUMBER: 03/180/997
PRIOR FILING DATE: 1997-05-03
PRIOR FILING DATE: 1997-05-03
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
COPTUADED: Datastrue
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TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-974-992-7
                                                                                                                                                                                                                                                                                                                                                                                    Requence 3, Application US/09974992
ENERAL INFORMATION:
APPLICANT: Mathlesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
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Matches 137; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 ISCNNSGROGDSASTNPADESARGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MACNINSGRDGNT-SANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSSIDEIAAK 59
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                           32.2%; Score 596.5; 66.0%; Pred. No. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.1%; Score 631; DB 6 69.9%; Pred. No. 1e-38;
       25; Mismatches
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                           . 2e-36
                                        DB 6;
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         38;
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                                        Length 207;
   Indels
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   Gaps
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1014
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1014
OTHER INFORMATION: Ceres Seq. ID 1836847
US-09-708-427-19883
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US-09-708-427-19883
; Sequence 19883, Application US/09708427
; GENERAL INFORMATION:
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Best Local Similarity
Matches 113; Conserv
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19883
LENGTH: 1014
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
270 GHNGTL-----LAGAYTISKLITQKLDGLK-NSEKLKEKIENAKKCSEDFTKKL--EG
                                            690 VEKLKTHENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                 234 VLAVKEIETLLASIDELATKAIG-----
                                                                                                                                 183 -TSPVVAESPKK------PSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAV 233
                                                                                                                                                                                   575
                                                                                                                                                                                                                         517 AEESLEQKG--REIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKL 574
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                                                                           -KKIQQNG----GLAVEA
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COCATION: 1..1018
OTHER INFORMATION: Xaa is any
NAME/KEY: misc_feature
LOCATION: 1..1018
OTHER INFORMATION: Ceres Seq.
US-09-708-427-19882
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: B5364
SOFTWARE: Patentin version 3.1
SEO ID NO 1982
LENGTH: 1018
TYPE: PRT
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Best Local Similarity
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                                                                                                      GHNGTL-----LAGAYTISKLITQKLDGLK-NSEKLKEKIENAKKCSEDFTKKL--ÈG
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EKLQSQIEKLRAVAAEKSVL-----ESHFEELEKTLSEVKAQLKENVENAATASVKVAE
                                        EHAQLGIENVTDENAKKAILITDAAKDKGAAELEK-----LFKAVENLAKAAKEM--
                                                                                                                                                             VEKLKTHENQIEEYKKLAHEASGVADTRKVELEDALSKLKNLESTIEELGAKCQGLEKES
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Pred. No. 0.00018;
8; Mismatches 161;
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; LOCATION: 1..1269
; OTHER INFORMATION: Ceres
US-09-708-427-19881
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-11243P
CUBRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19881
LENGTH: 1269
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Best Local Similarity
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OTHER INFORMATION: Xaa is any
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ORGANISM: Arabidopsis thaliana
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Pred. No. 0.00024;
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Sequence 3, Application US/09742096
GENERAL INFORMATION:
APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STIFLE REFERENCE: 200773USDIV
CURRENT APPLICATION NUMBER: US/09/742,096
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/73,642
PRIOR FILING DATE: 1998-02-06
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TYPE: PRT
; ORGANISM: P. falciparum
US-09-742-096-5
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GENERAL INFORMATION:
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
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CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/973,642
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: PCT/FR96/00894
PRIOR FILING DATE: 1996-06-12
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PRIOR FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                  516 VESNEKVAENLEKL 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 ESVAPSVEESVAEN----
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Similarity 18.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ----ITDAAKDKGAAELEKLFKAVENLA 363
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                                                                                               STAGE POLYPEPTIDE MOLECULES
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CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
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US-09-614-150-6213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6213, Application US/09614150 GENERAL INFORMATION:
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PRIOR FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1786
                                                               PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING TITLE OF INVENTION: DROSOPHILA GENES.
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                                                PRIOR
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PRIOR FILING DATE: 1996-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 VTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAES--P 191
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                     APPLICATION NUMBER: 60/184,831 FILING DATE: 2000-02-24
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18.7%;
60/191,637
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Pred. No. 0.0031;
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EXPRESSION OF 10,000 OR MORE
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NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ for Windows VG
SEQ ID NO 6213
LENGTH: 1639
TYPE: PRT
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US-09-708-427-3730
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-708-427-3730
                                                                                                                                   EMERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING |
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT FILLNG DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PACENTIN VETSION 3.1
SEQ ID NO 3730
LENGTH: 805
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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Best Local S
Matches 105
            NAME/KEY: misc_feature
LOCATION: 1.805
OTHER INFORMATION: Xaa is a
NAME/KEY: misc_feature
LOCATION: 1.805
OTHER INFORMATION: Ceres Se
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3730,
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les 105; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETFTNKLK-EKHTDLGKEGVTDADAKEAILKAN-----GTKTKG--AEELGK 159
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                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09708427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%; Score 159.5; DB 23.9%; Pred. No. 0.003;
                Seq.
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3729
LENGTH: 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3729, Application US/09 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                           Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1..841
OTHER INFORMATION: Ceres
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LOCATION: 1..841
                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                      67
                                                       86 VKHKELTEVKEAFDGLGLELENSRKKMIELEDRIRISALEAEKLEELQKQSASELEEKLK 145
                                                                                        21 VKGPNLTEINK-----KITDSNAVLLAVKE---VEAL----LSSIDEIAAKAIGKKIH
                                                                                                                             Local Similarity
nes 86; Conserv
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QNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKI-----
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FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..1038

OTHER INFORMATION: Xaa is any an NAME/KEY: misc_feature
LOCATION: 1..1038

OTHER INFORMATION: Ceres Seq. II
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US-09-708-427-32624
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Best Local Similarity
Matches 104; Conserv
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32624
LENGTH: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32624, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                              64 KIHQNNGLDTENNHNGSLLAGA-----YAISTLIKQKLDGLKNEGLKEKIDAAK--KC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 EAKDLITKLKSH-----ENVIEEH-KRQVLEASGVADTRKVEVEEALLKLNTLESTIEE 492
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NGEIIKPCEAKENREQPAKKSFTEEE-----AARIIQSMYRGYDVRRWEPIKKLKEIAT 593
                                     LANSVKELTSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLT--EISKKITESNA 232
                                                                             AAPLSSKKAESRTVPEACNVKCEDANAEMKMAEGSLNALRTEKG----SVESNSNLQEES
                                                                                                                                                        RIAKNEPVKSTKKEQSSSSSEASKLPPVCLRVDPLPKERNGGSKSVSHPKRMEKSKETKI 483
                                                                                                                 SETFTNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEM 174
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ilarity 25.0%; Pred. No. 0.0032;
Conservative 53; Mismatches 186;
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; Sequence 32623, Application US/09708427
; SENERAL INFORMATION:
; ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; FILE REFERENCE: 2750-1243P
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32623
LENGTH-1042
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                     488 AAPLSSKKAESRTVPEACNVKCEDANAEMKMAEGSLNALRTEKG----SVESNSNLQEES
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SDTNLEKVLRLSPEEHPMSVLNRTDEKQAESAAETEEGYGLFETLATDSKQATENA
                                                                          ALATELSSIQDKLDSLKNSCASAEKEAVKEQVEIKSQPSD---SPVNLEHSQLTEENKMV
                                                                                                                  GAYTISKLITQKLDGLKNS-----EKLKEKIENAKKCSEDFTKKLEGEHAQLGIEN--V 329
                                                                                                                                                        VREQMGDVKKRIEALEASTDQHIEE----KEIVVNGELVMNLLLKLDAVEGLHPSIREFRK 654
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                                   -TDAAKDKGAAELEKLFKAVENLAKAAKEMLANS
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NAME/KEY: misc_feature

LOCATION: 1..1043

OTHER INFORMATION: Xaa is any amino ac

NAME/KEY: misc_feature

LOCATION: 1..1043

OTHER INFORMATION: Ceres Seq. ID 18346

-09-708-427-32622
                                                                                                                                                                              Sequence 7646, Application US/10032585
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
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Best Local Similarity 25.0
Matches 104; Conservative
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 3622
LEUGTH: 1043
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7646
                                                                                                               APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies
FILE REFERENCE: 10182-005-999
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25.0%; Pred. No. 0.0032;
ative 53; Mismatches 186;
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; LOCATION: (1881)..(1881)
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TYPE: PRT
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                                    356 FKAVENLAKAAKEMLANSVKEL 377
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                                                                                 DDSKKKLTELENDLTSTKKELETEKTQTSKFKNLEER--
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LELLKNDNSGAKKELSEKVSKL 1855
                                                                                                                     IENAKKCSE---DFT---KKLEGEHAQLG-IENVTDENAKKAILITDAAKDKGAAELEKL 355
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Search completed: March 18, 2002, 09:58:21 Job time: 379 sec

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5	44	43	42	41	40	39	38	37	36	3 <u>5</u>	ω 4	ω ω	32	31	30
622.5	627	627	628	630	630.5	630.5	631	635.5	635.5	638	641.5	646	650	655	657.5
33.6	33.9	33.9	33.9	34.1	34.1	34.1	34.1	34.4	34.4	34.5	34.7	34.9	35.1	35.4	35.5
209	212	210	210	192	209	209	212	203	191	194	193	214	212	212	502
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S69926	S69921	S69923	S69925	S70285	I40285	I40281	S20543	I40108	S70288	S70289	S70286	S69916	I40143	I40279	140142
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 19-210 <LIV>
A; Cross-references: EMBL:L42887; NID:g858715;
A; Cross-references: strain Ip2
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R;Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu A;Reference number: 140269; MUID:96025162
A;Accession: 140269
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000
C;Accession: G70218; I40269; S37726; S70281
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                             A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X69596; NID:g311391; PIDN:CAA49306.1; PID:g311392 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448 A;Accession: S70281 A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-210 <RES>
A;Residues: 1-210 <RES>
A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684
A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684
A;Tauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, Med. Microbiol. Immunol. 182, 37-50, 1993
Med. Microbiol. Immunol. 182, 37-50, 1993
A;Title: Genetic heterogenity of the genes coding for the outer surface protein C A;Teference number: S37726; MUID:93268136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic Sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: G70218
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A; Residues: 1-210 <K
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A; Residues: 1-210 <JAU>
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Superfamily: Lyme disease spirochete surface
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Outer surface protein C precursor - Lyme disease spirochete (strain PKa)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Variety: Strain PKa
C;Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
C;Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
R;Jauris-Helpke, S; Liegi, G; Preac-Mursic, V; Roessler, D.; Schwab, E.; Sout
J; Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of
A;Reference number: 140047; MUID:95395018
A;Recession: 569927
A;Status: nucleic acid sequence not shown
A;Residues: 1-210 <JAU>
A;Cross:references: EMBL:X69589
A;Staprimental source: strain PKa
R;Jauris, S.
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A: Residues: 1-124,'D',126-139,'E',141-210 <JAW>
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A;Reference number: S72669
A;Accession: S72669
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Superfamily: Lyme disease spirochete surface protein
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                                                                          ELTSPVVAESPKKP 194
                                                                                                         KLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                  ELTSPVVAESPKKP 210
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                                                                                            KLKDKHTDLGKEGYTDADAKEATLKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
                                                                                                                                              IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIEAAKKCSETETN 136
                                                                                                                                                            IGKKIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLKNEGLKEKIDAAKKCSETETN 120
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97.98;
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Pred. No. 1.
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Pred. No. 5.5e-39;
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1.2e-38;
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                                                                                                                                                                                                                                                                                    Length 210
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A; Residues: 1-193 <LIV>
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178; Conserv
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A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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A:Residues: 1-191 <RES>
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R;Fung, B.P.; McHugh, G.L.; Leong, J.M.; Steere, A.C.
Infect Immun. 62, 3213-3221, 1994
A;Title: Humoral immune response to outer surface protein
A;Reference number: I40153; MUID:94314437
A;Accession: I40153
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Best Local Similarity 100.0%; Pred. No. 100.0%; Pred. 
318 EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 KIQONGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 121
                                                                                                                                              NSGKGGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKK
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99.4%;
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Pred. No. 4.2e-35;
0; Mismatches 1;
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Pred. No. 1e-35;
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outer surface protein C - Lyme disease spirochete (strain TXGW) (fragment) C;Specles: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-200(C;Accession: I40129; S54199 R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Har J. Bacteriol. 177, 3036-3044, 1995 A;Title: Evolution of the Borrelia burgdorferi outer surface protein OspC. A;Reference number: I40104; MUID:95286481 A;Accession: I40129
                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-178 <RES>
Cross-references: EMBL:X84779; NID:g793817; PIDN:CAA59250.1; PID:g793818
C;Superfamily: Lyme disease spirochete surface protein C
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A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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A;Molecule type: DNA
A;Resldues: 1-177 <ARES>
A;Cross-references: EMBL:X84783; NID:g793825; PIDN:CAA59254.1; PID:g793826
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Best Local Similarity
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Best Local (
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Matches 174;
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                                                                                                                                                                          205 NTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKKIQQNGG
  121
                                                                                                 265 LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
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                                                                                                                                                        1 NTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKKIQQNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLG 130
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GIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLPKAAKEMLANSVKEL
                                      GIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 377
                                                                           LAVEAGHNGTSLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
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                                                                                                                                                                                                                                                    Similarity
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98.3%;
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Pred. No. 1.1e-34;
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Pred. No. 2.3e-33;
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                                                                                                                                                                                                                                                                    Length 178;
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  173
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outer surface protein C - Lyme disease spirochete (strain 272) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000 C;Accession: 140104; S54184 R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Hans J. Bacteriol. 177, 3036-3044, 1995 A;Title: Evolution of the Borrelia burgdorferi outer surface protein OspC. A;Reference number: 140104; MUID:95286481 A;Accession: 140104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer
A;Reference number: I40143; MUID:95154673
A;Accession: I40145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Borrelia burgdorferi (Lyme disease spirochete C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C:Accession: I40145
                                                                                                                                                                                                                                                                                                                                                                                A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface
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C;Superfamily
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A; Residues: 1-178 <RI
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A; Residues: 1-211 <RES>
A; Cross-references: EMBL:U04282; NID:g2314881; PIDN:AAC45540.1;
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Best Local
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Best Local Similarity
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                                                                                                                                           AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFT 119
                                                                                                                      AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLITOKLGGLKNEELKEKIAAVKKCSEEFT
    KELTSPVVAESPKKP 194
                                         NKLKSSHTELGKQDAQDDDAKKAILRTHNTKDKGAEELDKLFKAVENLSKAAKEMLSNSV
                                                                               NKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSV
                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                   41.9%;
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Pred. No. 3.2e-33;
Pred. No. 3.2e-33;
                                                                                                                                                                                                                                                                                                   Score 774.5; DB Pred. No. 8.1e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from GB/EMBL/DDBJ
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_Change 26-:
C;Accession: I40124; S54194
R;Theisen, M.; Borre, M.; Machhiesen, M.J.; Mikkelsen, B.; Lebech, A
J; Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer surface protei
A;Reference number: I40104; MUID:95286481
A;Accession: I40124
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1178 <RES>
A;Cross-references: EMBL:X84782; NID:g793815; PIDN:CAA59253.1; PID:
C;Superfamily: Lyme disease spirochete surface protein C
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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
MOl, Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation: A;Reference number: $70255; MUID:96296448
A;Accession: $70279
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C;Superfamily: Lyme disease spirochete surface protein
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                                                                                                                                                   Query Match
Best Local
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Best Local S
Matches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA esidues: 1-193 <LIV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ross-references: EMBL:L42898; NID:g858729; Experimental source: strain 25015
  265
                                                                                             205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 LTSPVVAESPKKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LKEKHTDLGKEGVTDADAKEAILKANGTKTKGABELGKLFESVEVLSKAAKEMLANSVKE 181
                                                                                                                                                 Local Similarity
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LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL 324
                                                          NTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKKIQONGG 264
                                       NTSANSADESYKGPNLTEISKKITESNAGGLAVKEIETLLASIDELATRAIGKKIQQNGG
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58; Conservative
                                                                                                                               Conservative
                                                                                                                                             39.9%;
                                                                                                                                                                                                                                                                                                                                                                                               Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Hansen,
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81.9%;
                                                                                                                        Score 739; DB Pred. No. 3.3e.6; Mismatches
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Pred. No. 8.2e-31;
(1; Mismatches 23;
                                                                                                                                             DB 2;
.3e-29;
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                                                                                                                                                            Length 178
                                                                                                                      Indels
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                                                                                                                                                                                                                                         PID: 9793816
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Outer surface protein C precursor - Lyme disease spirochete (strain PBre) C.Species: Borrelia burgdorferi (Lyme disease spirochete)
A; Variety: strain pBre
C; Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000 C; Accession: S69918; 572674; I40103
R; Jauris-Heipke, S.; Liegl, G.; Preac-Mursic, V.; Roessler, D.; Schwab, E.; J. Clin. Microbiol. 33, 1860-1866, 1995
J. Clin. Microbiol. 33, 1860-1866, 1995
A; Title: Molecular analysis of genes encoding outer surface protein C (OspC)
A; Reference number: I40047; MUID:95395018
A;Reference number: 140047; MUID:95395018
A;Accession: S69918
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                          S69918
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C;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross references: EMBL:L42893; NID:g858721; A;Experimental source: strain 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U04281; NID:g434663; PIDN:AAC43297.1; R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and recombination in Ospa, Title: Evidence for lateral transfer and
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A; Residues: 19-210 <LIV>
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A; Accession: $70282
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A; Residues: 1-210 < RES>
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ilarity 75.4%;
Conservative 2
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Pred. No. 1.1e-27;
22; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAB37001.1;
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A; Residues: 1-211 <JAU>
A; Cross references: EMBL:X81522; NID:g872021; PIDN:CAA57242.1; PID. A: Experimental source: strain PBre
R; Roessler, D.
submitted to the EMBL Data Library, September 1994
A; Reference number: S72674
A; Accession: S72674
A; Molecule type: DNA
A; Residues: 1-152, 'E', 154-211 <ROE>
A; Cross-references: EMBL:X81522; NID:g872021; PIDN:CAA57242.1; PID C:GenetLos:
A; Gene: ospC
C; Superfamily: Lyme disease spirochete surface protein C
                                                                                                                                                                                                                                                                                                                                                                                        J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence analysis A;Reference number: I40269; MUID:96025162
A;Accession: I40277
A;Coression: T40277
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Best Local Similarity
Matches 146; Conserv
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                                                           VKELTSPVVAESPKKP 211
    VKELTSPVVAESPKKP
                                 VKELTSPVVAESPKKP 194
                                                                                                                       AIGQKI-QNNGLAAEADKNGSLLAGAYAISTLIKQKLDGLKGLEGLNKEIAEAKKCSEAF
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                                                                                                                                                                                                                                          Score 692.5; DB 2;
Pred. No. 6.9e-27;
90; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 695.5; DB 2
Pred. No. 4.9e-27;
2; Mismatches 29
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                                                                                                                                                                                                                                            27;
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Gene 143, 105-110, 1994
A.Title: Homology between Borrelia burgdorferi
A.Reference number: 140268; MUID:94259285
A;Accession: I40268
A;Status: preliminary; translated from GB/EMBL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
I40268
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Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination
A;Reference number: S70255; MUID:96296448
A;Accession: S70280
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                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-211 <RES>
A;Cross-references: GB:L25413;
C;Genetics:
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C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-193 <LIV>
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P24043 homo sapien
Q10410 streptcoccc
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Q10410 yrickettsia
P82094 homo sapien
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SEQUENCE FROM N.A. STRAIN-ATCC 35210, MEDLINE-96025162; Fukunaga M., Hamass "Outer surface prot burgdorferi sensu J. Clin. Microbiol. [5] SEQUENCE FROM N.A. STRAIN-ATCC 35210, MEDLINE-98065943; Fraser C.M., Casjen Lathigra R., White Dougherty B., Tomb Peterson J., Kerlay van Vugt R., Palmer	SEQUENCE FROM N.A. STRAIN-ATCC 35210 / R MEDLINE-93239332; Pul Wilske B., Preace-Mu Schwab E., Wanner G., "Immunological and me major outer surface I Infect. Immun. 61:218 [3] SEQUENCE FROM N.A. STRAIN-ATCC 35210 / I MEDLINE-94041630; Pul Padula S.J., Sampier. "Molecular character. "Molecular character." "Molecular strain of Be Infect. Immun. 61:50:	OSC1_BORBU STAND Q07337; 15-DEC-1998 (Rel. 37) 15-DEC-1998 (Rel. 37) 20-AUGC-2001 (Rel. 40) OUTER SURFACE PROTEI OSPC OR BBB19. BORTC-11a burgdorferi Plasmid 1p54. BACTETIA: Spirochaet NCBL TAXID-139; [1] ABDLINE=92368136; PU JAUTIS-Heipke S., FU Will G., Wilske B.; "Genetic heterogenit Protein C (OSPC) and Med. Microbiol. Immu [2]	5 139.5 6 139.5 6 139.5 7 139.5 9 138.5 9 137.5 137.5 137.5 137.5 137.5 137.5 137.5 137.5 137.5
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         Fuchs
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Nature 390:580-586(1997).

"I FUNCTION: NOT KNOWN, MAJOR IMMUNODOMINANT PROTEIN."

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                                                                                           Borrelia hermsii.
SEQUENCE FROM
                                NCBI_TaxID=140;
                                                  Bacteria; Spirochaetales;
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or send an email to license@isb-sib.ch).
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J. Clin. Microbiol. 31:2570-2576(1993).
i- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
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SEQUENCE FROM N.A.

STRAIN-SSP, HS1 SEROTYPE 3;

MEDLINE-93133110; PubMed-1484486;

Restrepo B.I., Kitten T., Carter C.J., Infante D., Barbour & Subtelomeric expression regions of Borrelia hermsii linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are highly polymorphic.";
Mol. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE
FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93133110: PubMed=1484486;
Restrepo B.I., Kitten T., Carter C.J., Infante D., Barbour A "Subtelomeric expression regions of Borrelia hermsii linear
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
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                                                                                                                                                                                                                                                                                        AEGEVEAAIKELTAPVKAEKPSQ 212
                                                                                                                                                                                                                                                                                                                   AKEMLANSVKELTSPVVAESPKK 193
                                                                                                                                                                                                                                                                                                                                              VKSKAEAFLNKLKDGHTELGKKDASDDDTKKAIKKDNSDKTKGASELEALNTAVDALLKA
                                                                                                                                                                                                                                                                                                                                                                                                    -AKAIGKKIKNDGGLDTEAGQNGSLIAGVHSVVSAVKIKVGALETTSGISNE-LKTKITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSCNNGGPE-----LKSDEVAKSDGTVLDLAKVSKKIKEASAFAASVKEVETLVKSVDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001800; Lipoprotein_6.
                                                                                              Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
214 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                   el. 26, Created)
el. 26, Last sequence update)
el. 28, Last annotation update)
oUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۶
                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
22541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO VMP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MΨ;
                                                                                              Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-ACYL DIGLYCERIDE; F1583F510246F7C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE.
VARIABLE MAJOR OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPOPROTEIN
                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397.5; DB 1;
. No. 3.2e-12;
                                                                                                                                                                                                                     215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
                                                                                                Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ָי.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROBABLE)
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbour A.G.;
                Barbour A.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHANGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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 plasmids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYSN_ACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 92
          01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
MYOSIN II HEAVY CHAIN, NON MUSCLE.
Acanthamoeba castellanii (Amoeba).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are highly polymorphic.";

Mol. Microbiol. 6:3299-3311(1992).

-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.

-i- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87308395; PubMed=3040773;
Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L04789; AAA22967.1; -.
InterPro; IPR001800; Lipoprotein_6.
                                                                                                                                                      Eukaryota; Acanthamoebidae; Acanthamoeba
                                                                                                                                                                                                                                                                MYSN_ACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01441; Lipoprotein
                                                                                                                                                                                                                                                                                                                                191
                                                                                                                                                                                                                                                                                                                                                          171
                                                                                                                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                                                                                                                                                                                                                       72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MACNNSGKDGNTSANSADESVKGP----NLTEINKKITDSNAVLLAVKEVEALLSSIDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: STRONG, TO VMP24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAKAIGKKI-HONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLK-----NEGLKEKIDA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSCNNGGPE-----LKSDEVAKSDGTVLDLAKISKKIKDASDFAASVKEVHTLVKSIDEL
                                                                                                                                                                                                                                                                                                                                ANDAVETVIKELTASVKAEKPSQ
                                                                                                                                                                                                                                                                                                                                              AKEMLANSVKELTSPVVAESPKK
                                                                                                                                                                                                                                                                                                                                                                                                  AKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKA
                                                                                                                                                                                                                                                                                                                                                                                    VKKESEAFVTQVKSKHTDLAKEGVTDAHAKSAILVTDGTKDKGAAELIKLNTAIDELLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                      -AKAIGKKIKNDNSNFEDENDHNGSLIAGVFQVILTVKAKLTSLEQIIGISDELKTEVGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
92; Conserv
FILAMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
215
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23139
HEXAMER OF 2 HEAVY CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 397; DB 1;
Pred. No. 3.4e-12;
5; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIABLE MAJOR OUTER MEMBRANE LIFOPROTEIN 3. N-ACYL DIGLYCERIDE (PROBABLE); 684C74D35F87C771 CRC64;
                                                                                                                                                                                                                                                                                                                                213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE
                                                                                                                                                                                                                                                                PRT;
                                                                          deduced polypeptide from Acanthamoeba: e
                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid
             TWO-HEADED.
                                      TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 215
                                      F-ACTIN
             IT SELF-ASSEMBLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                              evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
(MHC),
                                                                                         sequence
                                       80
                                       HAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                            of of
 ALKALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                    190
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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InterPro; IPRO01609; myosin_head.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOm; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00015; IQ; 1.
SMART; SM000242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                       187
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DOMAIN
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PROSITE; PS50096; IQ; 1.

Myosin; Coiled coil; Actin-binding; ATP-binding; Calmodulin-binding;
Myosin; Coiled coil; Actin-binding; Miltigene family.

Methylation; Alkylation; Phosphorylation; Multigene family.

MYOSIN HEAD-LIKE.
                                                                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00624; CAA68663.1; -. PIR; A27224; A27224. HSSP; P08799; 1MND.
                                                                                                                                                                                                                                991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab-
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
KSKLSAAEKSLKTAKDQNRDLDEQLEDERTYRANYDKQKKALEAKLTELEDQYTALDGQK 1166
                                                                                                     DDVTATKLQLEKTKKSLEEELAQTRAQLEE-EKSGKEAASSKAKQLGQQLEDARSEVDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.

MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                 ----VAESPKKPSMVNNSG-----KDGNTSANSADESVKG--PNLTEISKKIT---
                                                                                                                                                         -DAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPV------
                                                                                                                                                                                                             YEDEAAAHDSLKKKEEDLSRE-LRETKDALADAENISETLRSKL--KNTERGADDVRNEL
                                                                                                                                                                                                                                                         LAGAYAISTLIKOKLDGLKNEGLKEKIDA---AKKCSETFTNKLKEKHTDLGKEGYTDA-
                                                                                                                                                                                                                                                                                                               ELQEETSASNDILEQKRKLEAEKGELKASLEE---EERNRKALQEAKTKVESERNELQDK 990
                                                                                                                                                                                                                                                                                                                                                                 EINKKITDSNAVLLAVKEVEA----LLSSIDEIAAKAIGKKIHO--NNGLDTENNHNGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1483
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    819
1509
1226
1252
1509
1482
1509
1489
189
682
780
133
700
1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171201
                                                                                                                                                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 174.5;
Pred. No. 0.38
73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQ.
COILED COIL (POTENTIAL).
ATOHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-HELICAL TAILPIECE (LMM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONHELICAL TAILPIECE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGHT MEROMYOSIN (LMM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2CE49BE51173D17E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          159;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                       67;
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                                                      -ES
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                                                                                                          1106
                                                                                                                                                                                                             1047
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RESULTANT OF THE PRESULT OF THE PRES
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                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, C
01-FEB-1991 (Rel. 17, L
15-JUL-1999 (Rel. 38, L
M PROTEIN, SEROTYPE 5 P
                                                                                    Transmembrane;
                                                                                                                                                                             Pfam; PF00746; Gram_pos_anchor; Pfam; PF02370; M; 9.
                                                                                                                                                                                                                                                                                PIR;
PIR;
                                                                                                                                                                                                                           InterPro; IPR001899; Gram_pos_anchor
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol.
                                                                                                             Virulence;
                                                                                                                                       PROSITE;
                                                                                                                                                         PRINTS; PR00015; GPOSANCHOR
                                                                                                                                                                                                                                                                                                                            EMBL; M20374; AAA26976.1;
                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller L., Gray L., Beachey E., Kenoe m.;
"Antigenic variation among group A streptococcal M proteins."
"Nucleotide sequence of the serotype 5 M protein gene and its
Nucleotide sequence of the serotype 5 M protein gene and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptococci.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 43-212 AND 238-250.
MEDLINE=84162039; PubMed=6368549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M5_STRPY
P02977;
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J. Biol. Chem. 263:5668-5673(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197-residue fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMM5 OR SMP5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE BACTERIUM AND CAN RENDER THE ORGAN
PHAGOCYTOSIS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE
SUBLARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND
                                                                                                                                                                                                                                                                           A03501; MMSOMP.
A28616; A28616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERVICE OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS PROTEIN IS ONE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ula B.N., Acharya A.S., Mische S.M., Fairwell T., Fischetti complete amino acid sequence of a biologically active residue fragment of M protein isolated from type 5 group A
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                                                                                                                                  PS00343;
                                                                                                   S00343; GRAM_POS_ANCHORING; Phagocytosis; Cell_wall; D
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                                                                                 Coiled coil;
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, Beachey E., Kehoe M.;
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M PROTEIN, SEROTYPE 5.
EXTRACELLULAR (POTENTIAL).
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Best Local Similarity 24.9
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REPEAT
                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B A
                                                                                          Streptococcus, NCBI_TaxID=1311;
                                                                                                                              Streptococcus agalactiae
Bacteria; Firmicutes; Bac
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                     medLINE-91312121; PubMed-1857207;
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 P.G., Chhatwal
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CYTOPLASMIC (POTENTIAL).

GLY/PRO-RICH (CELL WALL-SPANNING)
CONSERVED IN GRAM-POSITIVE COCCI (
PROTEINS.

5 X 7 AA TANDEM REPEATS OF L-K-T-I
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N -> S (IN REF. 2).
K -> SNLERKTAELTSEK.
I -> L (IN REF. 2).
87377986CBD55E27 CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bateman A., Eddy S.R., Chothia C.; "Members of the immunoglobulin superfamily Protein Sci. 5:1939-1942(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X59771; CAA42442.1;
PIR; S15330; FCSOAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: TYPÉ I MEMBRANE PROTEIN. CELL WALL.
-i- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
-i- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The IgA-binding beta antigen of the streptococci: sequence determination
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00746; Gram_pos_anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001899; Gram_pos_anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97035265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 5:843-849(1991).
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378
                      289
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                                                                                                                                                                                              187
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                                                                                                            TSPVVAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVL------
                                                                                                                                                            KEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL
                                                                                                                                                                                               TKVDLSN-IDKELNHQKS-
                                                                                                                                                                                                                                                          SGKDGNTSANSADESVKGPNLTEINKKITDSNAVLLAVK---EVEALLSSIDEIAAKAIG
KLNQSKNLPELKQLEEEAHSKLKQVVEDFRKKFKTS-----
                      KLDGLKNSEKLKEKIENA----KKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAA
                                                                                              DQEIQEHVKKETSSEENTQKVDEHYANSL-QNLAQKSLEELDKATTNEQATQVKNQFLEN
                                                                                                                                             LKKIEDIRKQ-AQQADKKE-----DAEVKVREELGKLFSS----TKAG------L
                                                                                                                                                                                                                     KKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL
                                                                                                                                                                                                                                             SHEQKNEFKTKIDETNDSDALLELENQFNETNR-LLHIKQHEEVEKDKKAKQQKTLKQSD
                                               AQKLKEIQPLIKETNVKLYKAMSESLEQ----VEKELKHNSEANLEDLVAKSKEIVREYEG
                                                                      --AVKEIETLLASIDELATKAIGKKIQQNGGLAVEAGHNG----TLLAGAYTISKLITQ
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                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                         1164
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1141
1160
434
199
439
827
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                                                                                                                                                                                                                                                                                                         8.9%;
                                                                                                                                                                                                                                                                                                                                                         131051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
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                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                   Score 164.5;
                                                                                                                                                                                                                                                                                                                                                                              IG-LIKE DOMAIN.
IGA-BINDING (POTENTIAL).
IGA-BINDING (POTENTIAL).
PRO-RICH REPEATS.
CONSERVED IN GRAM-POSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                           IGA FC RECEPTOR.

EXTRACELLULAR (POTENTIAL).

MEMBRANE ANCHOR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                     PROTEINS
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                                                                                                                                                                                                                                                                                                                                                         65DE94AF720A5474 CRC64;
                                                                                                                                                                                                                                                                                                         NO.
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 -EQVTPKKRVKRDL--
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                                                                                                                                                                                               -KDSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collaboration -
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                        344
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428
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RESULT 8
USO1_YEAST
ID USO1_YEAST
AC P25386;
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                                                                                         DOMAIN
                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                  EMBL; X54378; CAA38253.1; -. EMBL; L03188; AAB00143.1; -. EMBL; U53668; AAB66659.1; -.
                                                                                                                               DOMAIN
                                                                                                                                                       InterPro;
                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=X2180-1A;
MEDLINE=91185402; PubMed=2010462;
MEDLINE=91185402; PubMed=2010462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kendrick K.E.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 782-1790 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
USO1 OR INTI OR YDL058W. 'Palen'' (Palen')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hostetter M.K., Herman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakajima H., Hirata A.,
Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A cytoskeleton-related gene, uso1,
                                                                                                                                                    P; P80220; 1DIP.
; S0002216; USO1.
erPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429
                                                                                                                                                                                                                                                                                                                                                  MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.

ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COLLED COLLS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otein transport in Saccharomyces Cell Biol. 113:245-260(1991).
                                                                                                                                                                                          A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL
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924
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                                                                                                                                      transport;
                                                                                                                                                 Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.J.,
GLOBULAR HEAD.

COLLED COIL (POTENTIAL).

CHARGED (HYPER-HYDROPHILIC).

DISPENSABLE FOR THE PROTEIN FOR ASP/GLU-RICH (ACIDIC).

G -> E (IN REF. 2).

Y -> I (IN REF. 2).

I -> V (IN REF. 2).

I -> V (IN REF. 2).

I -> S (IN REF. 2).
                                                                                                                         Golgi stack; Cytoskeleton; Coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendel C.M., McClellan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yonehara T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , is required cerevisiae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is
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Best Local
CHICK
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                                              1325
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                                                                                                                                                                                                                                                                          1045
                                                    342 DAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                           3 CNNSGKDG------NTSANSADESVKGPNLTEINKKITDSNAVLLAVKEVEALLSS
                                    --AKEKSESELSRLKKTSSEERKNAEEQLEKLKNEI 1358
                                                                                                                           IDALNLQIKELKKNETNEASLLESIKSVESETV--KIKE---LQDECNFK------
                                                                                                                                                                                                                 LETSEKALKEVKENEEHLKEEKIQLEKEATETKOQLNSLRANLESLEKEHEDLAAQLKKY 1164
                                                                              -EKEVSELEDKLKASEDKNSKYLELQKESEKIKEELDAKTTELKIQLEKITNLSK-----
                                                                                                  ISKLITOKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILIT
                                                                                                                                              SNAVVLAVKEIE-----TLLASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYT
                                                                                                                                                                     EEQIANKERQYNEEISQLNDEITSTQQENESIKKKNDELEGEVKAMKSTSEEQSNLKKSE
                                                                                                                                                                                          KEMLANSVKELTSPV--VAESPKKPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITE 229
                                                                                                                                                                                                                                                  ADAKEAILK
                                                                                                                                                                                                                                                            SDSSKDEYESQISLLKEKLETATTANDENVNKISELTKTREELEAELAAYKNLKNELETK 1104
                                                                                                                                                                                                                                                                                       VEESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIEKNIEQLKKTISDLEQTKEEIISK
                                                                                                                                                                                                                                                                                                                               IDEIAAKAIGKKIHQNNGLD--TENNHNGSLLAGAY-----AISTL----IKQK
                                                                                                                                                                                                                                                                                                                                                     CNNLSKEKEHISKELVEYKSRFQSHDNLV--AKLTEKLKSLANNYKDMQA--ENESLIKA 984
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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1600
1661
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1790
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1600
1661
1772
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500 I -
561 R -
772 D -
206424 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 161.5;
Pred. No. 1.
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-> V (IN RE
-> S (IN RE
-> DEEDDEE
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> S (IN REF. 2).
-> V (IN REF. 2).
-> S (IN REF. 2).
-> DEEDDEE (IN REF. 6CE2B216E9FD4818)
                                                             377
                                                                                                                                                                                                                                                                                                                                                                                                                 .8;
                                                                                                                                                                                                                                                                                                                                                                                                      178;
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CRC64;
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REST_CHICK STANDARD,
042184; 042228; 057563; 057564;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 41, LAST ANNOTATION (CLIP-170).
TISSUE=Pectoralis muscle;
Griparic L., Keller T.C. III;
                                                                          SEQUENCE OF 17-1139 FROM N.A.
                                                                                               Griparic L., Volosky J.M., "Cloning and expression of Gene 206:195-208(1998).
                                                                                                                           SEQUENCE FROM N.A. MEDLINE=98137792; PubMed=9469933;
                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                    Archosauria;
                                                                                                                                                                                      Aves;
                                                                                                                                                                                  Neognathae;
                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                         Keller T.C. III;
chicken CLIP-170
                                                                         (CLIP-170(11) AND
                                   two novel CLIP-170/Restin
                                                                                                         and
                                                                      CLIP-170(11+35)).
                                                                                                        restin
          ASSOCIATED PROTEIN
  (BY SIMILARITY)
                                                                                                       isoforms.";
                                                                                                                                                                              Phasianinae;
                                         isoforms
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Query Match
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EMBL; AF020764; AAC60345.1; -.
EMBL; AF04565; AAC03547.1; -.
EMBL; AF04565; AAC03548.1; -.
EMBL; AF045651; AAC03548.1; -.
InterPro; IPR000938; CAP-Gly.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF01302; CAP_GLY; 2.
SMART; SM00343; Znf_C2HC; 1.
PROSITE; PS00845; CAP_GLY_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                              KAIGKKIQQNGGLAVEAGHNGTL----LAGAYTISKLITQKL-DGLKNSEKLKEKIENAK
                                                                                                                                                                                                                                                                                                                                                                EINKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDTENNHNGSLLAGAYA
                                                                                                                                                                                                                                           KPSMVNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELAT
                                                                                                                                                                                                                                                                                      GVGAQTAEFAELKTQMEKVKLDYE--NEMSNLKLKQENEKSQHLKEIEALKAKLLEVTEE
                                                                                                                                                                                                                                                                                                                          GVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAESPK
NLAKAAKEML 370
                                                                                                                    KLIGSLTQQ-----IRASEEKLLDLAALQKANSEGKLEIQKLSEQLQAAEKQIQNLETEK
                                                                                                                                                                                                     KEQTLEN-----LKAKLESVEDQHLVEMEDTLNKLQEAEIKVKELDVLQAKCNE-QT
                                                                                                                                                                                                                                                                                                                                                                                                           ISTL-IKQKLDGLKNEGLKEKIDAAKK----CSETFTNKLKE---KHTDLGKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSKHIDDVDTSLSLLQEI----SSLQEKMA-AAGKE-HQREMSSLKEKFESSEEALRKE
                                                                              KCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAEL----EKLFKAV---E
                                        -- VSNLTKELQGKEQKL-
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25.9%;
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CCHC-BOX.

MISSING (IN SHORT ISOFORM).

TOTKLEHARIKELEQSLLFEKTKADKLQRELEDTR ->
RKRQISEDPEN (IN ISOFORM CLIP-170(11)).

S -> GGSKVS (IN ISOFORM CLIP-170(11)).

T -> RKRQISEDPENT (IN ISOFORM CLIP-
170(11+35)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
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                                        -LDLEKNLSAVNQVKDSLEKELQLLKEKFTSAVDGAE
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Pred. No. 1
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-> V (IN REF. 2; AAC03548).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5631CE8683498E23 CRC64;
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5 5 5 5

S B

В

S

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RESULT 10
LMG1_DROME
                                          RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X., RA George R.A., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agabayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Bertova D., Botchan M.R., Bouck J., Brockstein P., Brottler P., RA Borkova D., Buschan M.R., Bouck J., Brockstein P., Brottler P., RA Dodson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Reischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Flaschman W., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Hortis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Lasko P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Pacleb J.M., Nelson D.L., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Rainer K., Kenter E., Wang A.H., Wang X., Stale R., Wang Y.-Y. W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p15215; Q24373; Q9VT18;
01-APR-1990 (Rel. 14, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN).
LANB2 OR LAMC1 OR LAMG1 OR CG3322.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CANTON-S, AND OREGON-R;
MEDLINE=91299161; PubMed=1840513;
Chi H.-C., Juminaga D., Wang S.Y.,
"Structure of the Drosophila gene in DNA Cell Biol. 10:451-466(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Montell D.J., Goodman C.S.,
Montell D.J., Goodman C.S.,
"Drosophila laminin: sequence of B2
three subunits during embryogenesis.
T Cell Biol. 109:2441-2453(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chi H.-C., Hui C.-F.;
Primary structer of the Drosophila laminin B2 chain and comparison with human, mouse, and Drosophila laminin B1 and B2 chains.";
J. Biol. Chem. 264:1543-1550(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BERKELEY;
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STANDARD;
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                                                                                                                                                                                                                                                                                           K.A.,
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S.M., R.-E.,

"cDNA and

Hui C.

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FlyBase; FB9n0002528; LanB2.
InterPro; IPR000561; EGF-like.
InterPro; IPR0001886; LanMT.
InterPro; IPR000034; Laminin_B.
InterPro; IPR000034; Laminin_B.
InterPro; IPR002049; Laminin_BGF.
Pfam; EP00053; laminin_BGF; 10.
Pfam; PF00053; laminin_BGF; 10.
Pfam; PF00055; laminin_BGF; 10.
Pfam; PF00058; Laminin_B; 1.
ProDom; PD002082; Laminin_B; 1.
ProDom; PD002082; Laminin_B; 1.
SMART; SM00180; EGF_Lam; 10.
SMART; SM00001; EGF_like; 1.
SMART; SM000281; LamB; 1.
SMART; SM00186; LamB; 1.
SMART; SM00186; LamB; 1.
SMART; SM00186; EGF_L; 8.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                PROSITE; PS00022; EGF_1; 8.
PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "CDNA and amino acid sequences of Drosophila laminin B2 chain.";
Nucleic Acids Res. 16:7205-7205(1988).

-i FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING ENTRY ONLY ENTRY OF THE EXTRACELULAR MATRIX COMPONENTS.

-i SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE TO EACH OTHER BY DISULTIDE BONDS INTO A CROSS-SHAPED MOLECULE TO EACH OTHER BY DISULTIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

-i SUBCELLULAR LOCATION: BASEMENT MEMBRANES (MAJOR COMPONENT).

-i DOMAIN: THE ALPHA HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT DOMAIN: THE ALMININ OF FORM A COILED COIL STRUCTURE.

-i SIMILARITY: CONTAINS I LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

-i SIMILARITY: CONTAINS 1 LAMININ EDGET-LIKE DOMAINS.

-i SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M58417; AAA28665.1; --
EMBL; M25063; AAA28664.1; --
EMBL; AE003551; AAF50238.1; --
EMBL; X07806; CAA30665.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=OREGON-R;
MEDLINE=88303364; PubMed=3405777;
Chi H.-C., Hui C.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 344-1639 FROM N.A.
                                                                                                                                                                                                                                                    Basement membrane, ike domain; Cell ad
                           LAMININ GAMMA-1 CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (V).
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ DOMAIN IV.
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                                                                                                                                                                                                                                            Extracellular matrix;
hesion; Repeat; Signal.
                         N EGF-LIKE 1.
N EGF-LIKE 2.
N EGF-LIKE 3.
N EGF-LIKE 4.
N EGF-LIKE 5 (N-TERMINAL).
N DOMAIN IV.
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Best Local S
Matches 105
1211 RALADKLESEAQFDLKNA----KDAKDAVEKAHQLAKSAIDLQLKIGTELRSEVGLELSH
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Pred. No. 2;
8; Mismatches
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PIR; A31483; MMFFB2. HSSP; P02468;

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                                                                                                                                                                                                                                                                                      EMBL; Z70690; CAA94624.1;
Hypothetical protein.
SEQUENCE 1957 AA; 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databasses.
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Schizosaccharomyces.
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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TDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAA
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PRINTS; PRO0015; GPOSANCHOR.
PROSITE; PS00343; GRAM_POS_ANCHORING;
Virulence; Phagocytosis; Cell wall; Du
Transmembrane; Coiled coil; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-85166224; PubMed-3885219;
Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
Scott J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
"Relationship of M protein genes in group A streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 82:1822-1826(1985).
-1- FUNCTION: THIS PROTEIN MIS CLOSELY ASSOCIATED WITH VIRULENCE OF PROTEIN MIS PROTEIN MIS CLOSELY ASSOCIATED WITH VIRULENCE THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
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MEDLINE=86111835; PubMed=3511046;

MEDLINE=86111835; PubMed=3511046;

Hollingshead S.K., Fischetti V.F., Scott J.R.;

Monplete nucleotide sequence of type 6 M protein of the Streptococcus. Repetitive structure and membrane anchor. "

J. Biol. Chem. 261:1677-1686(1986).
                                                                                                                      InterPro; IPR001899; Gram_pos_anchor
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                            entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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20-AUG-2001
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collaboration -

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MEDIINE-90349606; PubMed-2117279;
Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.;
"Complete sequence of the Drosophila nonmuscle myosin heavy-chain transcript: conserved sequences in the myosin tail and differential splicing in the 5' untranslated sequence.";
Proc. Matl. Acad. Sci. U.S.A. 87:6316-6320(1990).
-!- FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994
01-JUN-1994
20-AUG-2001
                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atches 92;
                                                                                                                                                                                                      TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seguence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROT
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 TDQNKNLTTENK---ELKAEENRLTT------ENKGLTKKLSEAE---EEAANKERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKLTEKEK----AELQAKLEAE---AKALKEQLAKQAEEL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTAELDKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSKLAALEKLNKELEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITQKLDGLKNSEK------LKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVKDKIAREQKSKQDIGALKQELAKKDEGNKVSEASRKGLRRDLDASREAKKQVEKDLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLLASI-----DELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KIAKEQESKETI------GTLKKTLDETVK----DKIAKE-QESKETIGTLKKILDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKEAIGTLKKTLDETVKDKIAKEQESK----ETIGTL-----KKTLDETVKD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHTDLGK-EGVTDADAKEATLKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNDKLTTENNNLTDQN---KNLTTENKNLTDQNKNLTTENK-------NL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43
458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀΑ,
                                   REQUIRED FOR MORPHOGENESIS AND
                                                                                                                                                                                                                                                                                                                                                                       NON-MUSCLE
                                                                                                                                                                                                                                                                                      Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411
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23.0%;
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4; Mismatches 144;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                           (ZIPPER PROTEIN) (MYOSIN II).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5 X 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMIN
BLOCKS SEPARATED BY 15 AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLY/PRO-RICH (CELL WALL-SPANNING).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
10 X 7 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROPHILIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE ANCHOR
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.67;
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a; Brachycera; Muscomorpha;
                         RESPONSIBLE FOR SIS AND CYTOKINESIS.
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                                                                                                      differential
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Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 1.
PROSTRE: SM000242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             1271
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SEQUENCE
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DOMAIN
NP_BIND
DOMAIN
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InterPro; FR000048; IQ.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001699; myosin_head.
Pfam; PF00612; IQ; II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                10 GNTSANSADESVKGPNLTEIN------KKITDSNAVLLAVK--EVEALLSSIDEIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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PIR; B36014; B36014.
HSSP; P08799; 1MND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M35012; AAA28713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (s or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- ALTERNATIVE PRODUCTS: 2 ISOFORWS; A LONG FORM (SHOWN HERE) SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                       QQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEK----IENAKKCSEDFTK
                                                                                                                                                        KRLNK---DIEALEROVKELIAQNDRLDKSKKKIQSELEDATIELEAQRTKVLELEKKOK
                                                                             NFDKILAEEKAISEQIAQERDTAEREAREKETKVLSVSRELDEAFDKIEDLENK----RKT
                                                                                                                NTSANSADESVKGPNLTE----ISKKITESNAVVLAV-KEIETLLASIDELATKAIGKKI 259
                                                                                                                                                                                            EELGKLFESVEVLSKAAKEMLANSVK------ELTSPVVAESPKKPSMVNNSGKDG
                                                                                                                                                                                                                                        SEKEALQEQLEEDDEAKRNYERKLAEVTTQMQEIKKKAEEDADLAKEL---
                                                                                                                                                                                                                                                                           -KNEGLKEKIDAAKKCSETFTNKLKEKHT---DLGKEGVTDAD-AKEAILKANGTKTKGA 154
                                                                                                                                                                                                                                                                                                               KLQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQQLLEEETRQKL-GLSSKLRQIE 1386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
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Alternative
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2017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 151.5;
Pred. No. 5.
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GLOBULAR TAILPIECE.
MISSING (IN SHORT ISOFORM).
MW; 73E3CB02BA8F2528 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REACTIVE SULFHYDRYL/ACTIN-BINDING LIGHT MEROMYOSIN (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 KDA/50 KDA JUNCTION 50 KDA/20 KDA JUNCTION ACTIN-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled coil; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
-ELDDLANTQGTADKNVHELEKAKRALESQLA 1586
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MYSN_DROME
ID MYSN_D
AC 099323
DT 01-JUN
DT 01-JUN
DT 20-AUG
DE MYOSIN
GN ZIP.
OS DIOSOP
OC Pterry
OC OCC
CC -i-FU
CC CC CC

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367

307 286

247 242 201 184 158

65 73

MYSN_DROME Q99323;

123; 2017;

Gaps

19;

58

99

1552

1438 204

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RESULT 14

MYS_AF
ID MYS_A
AC P2473
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DT 01-MA
DT 20-AU
DE MYOSI
OS AGGIL
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-MAR-1992 (Rel. 21, Created)
Ol-MAR-1992 (Rel. 21, Last sequence update)
20-AMG-2001 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, STRIATED MUSCLE.
Aequipecten irradians (Bay Scallop).
Eukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of the regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nyitray L., Goodwin E.B., Szent-Gyorg "Nucleotide sequence of full length c muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Adductor muscle; MEDLINE-91088319; PubMed-2263488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Adductor muscle;
MEDLINE-92011595; PubMed-1917970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1647
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                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nyitray L., Goodwin E.B., Szent-Gyoergyi A.G.; "Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation."; "Capable Chem. 266:18469-18476(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Houdusse A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94173332; PubMed=81
                                                                                                                                                                                                                                                                                                                                                                      Nature 368:306-312(1994)
                                                                                                                                                                                                                                                                                                                                                                                      resolution.
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X55714; CAA39247.1;
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ill length cDNA for
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Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00015; IQ;
SMART; SM00242; MYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1SCM; 30-APR-94.
PDB; 1WDC; 11-JUL-96.
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                                                                                                                                                                                                                                                                                    324 LGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVEN
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A40997; A40997
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E; PS50096; IQ;
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Spectrin.
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Pred. No. 6
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ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SI
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ALKYLATION (SH-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166;
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12;

21-JUL-1986 21-JUL-1986 20-AUG-2001

(Rel.

01, Created)
01, Last sequence update)
40, Last annotation updat

update)

NISOYM

HEAVY

(MHC B).

CAEEL

P02566; MYSB.

CAEEL

STANDARD;

1966

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C -!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
C -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
C HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
C AND 2 REGULATORY LIGHT (TARIN SUBUNITS) (MLC-2).
C -!- SUBCELULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
C -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
C YCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
C -!- PIM: TWO CYSTEINE RESIDUES IN THE 51 DOMAIN ARE SELECTIVELY
C -I- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
C SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              SMART; SM00242; MYSc; 1. Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                            Pfam; PF01576; myosin_head; 1. Pfam; PF01576; myosin_tail; 1.
                                                                                                                                                     ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J01050; AAA28124.1;
EMBL; V01494; CAA24738.1;
PIR; A02992; MWKW.
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MEDLINE-83273600; PubMed=65/035*,
Karn J., Brenner S., Barnett L.;
Protein structural domains in the Caenorhabditis elegans unc-54
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                          DOMAIN
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InterPro: IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS ELEGANS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nonsense mutations via altered transfer Cell 33:575-583(1983).
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"Periodic charge distributions in the myosin rod amino acid sequence match cross-bridge spacings in muscle.";
Nature 299:226-231(1982).
[3]
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Rhabditidae; Peloder
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Caenorhabditis elegans.
                                                                                                                                                                                                                                              PR00193; MYOSINHEAVY. PD000355; myosin_head
         851
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                                                                                                                                                     Methylation;
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Peloderinae; Caenorhabditis.
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                                                                                                                                                                     Coiled coil; Thick filament; Actin-binding;
                                                                                     Alkylation; Multigene family.
MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL).
HINGE.
LIGHT MEROMYOSIN (LMM)
                                                       ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnett L., Bolten
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                                                                                                                        244
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                                                                                                                                                                                                                                                                  70
EQRNGADTREQFFNAEKRATLLQSEKEELLVANEAAE
                        AKDKGAAELEKLFKAVE - - NLAKAAKE - - MLANSVKE
                                                                   KLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDA
                                                                                           RAQVEVSQIRSEIEKRIQEKEEEFENTRKNHARALESMQASLETEAKGKAELLR-----
                                                                                                                       LASIDELATKA-IGKKIQQ-
                                                                                                                                                                                                              LGKEGVTDADAKEAILKANGT---KTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP 185
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                                                 -- IKKKLEG
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
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Pred. No. 6.
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Best Local Sim
Matches 190;
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Q9S3P3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Microbiol. 18:257-269(1995).
EMBL; L42887; AAB35995.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Spirochaetales; NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyme disease Borrelia.";
Mol. Microbiol. 18:257-269(1995).
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"Evidence for lateral transfer and
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123 KEKHTDLGKEGVTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 182
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Pred. No. 2.6e-37;
1; Mismatches 1
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O1-FEB-1997 (TrEMBLrel. 02, Created)
O1-FEB-1997 (TREMBLrel. 02, Last seq
O1-JUN-2001 (TREMBLREL. 17, Last and O1-JUN-2001 (FRAGMENT)).
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Best Local (
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Q9R7B1;
Q9R7B1;
                                                                                              01-MAY 2000 (TremBLrel. 13, Created)
01-MAY 2000 (TremBLrel. 13, Last sequence update)
01-JUN-2000 (TremBLrel. 17, Last annotation updat)
00TER SURFACE PROTEIN C (FR.GMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel
                      MEDLINE=97478003; PubMed=9336916;
Ras N.M., Postic D., Foretz M., Baranton G.;
"Borrelia burgdorferi sensu stricto, a bacte
U.S.A.'?";
                                                              STRAIN-TETS
                                                                    SEQUENCE FROM N.A.
                                                                                          NCBI_TaxID=139;
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NCBI_TaxID=139;
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         Syst.
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                                                                                                                                               ProDom;
                                                                                                                                                     InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                           EMBL; AF029860; AAB86543.1; -
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Bacteria; Spirochaet
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                                                                                                                                                                                                                                         STRAIN=OC1
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InterPro; IPRO01800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1.
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SEQUENCE FROM N.A.
STRAIN=TETS;
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IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
                   ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKEKHTDLGKEGYTDADAKEAILKANGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186;
                                                                        Similarity
                                                                                                                                             PD001149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                      151:15-30(1999)
                                                                                                                                                                                                                                                                              Spirochaetales;
                                                                                                                193
193 /
                                                              Conservative
                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
CE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AA;
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                           Lipoprotein_6; 1.
                                                                                                              193
20502
                                                                      49.18;
97.98;
                                                                                                                                                                                                                                                                                        (Lyme
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97.9%;
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                                                                                                                MW.
                                                                                                                                                                                                                                                                              Spirochaetaceae;
                                                        Score 908; DB
Pred. No. 1.1e
3; Mismatches
                                                                                                                                                                                                                                                                                       disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 921; DB Pred. No. 2.7e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ψ
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                                                                                                              5EFDB5AFF8986D1E CRC64;
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                                                        e 908; DB 2; Le.
No. 1.1e-35;
                                                                                                                                                                                                                Dunn J.J.,
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.7e-36;
                                                                                                                                                                                                                                                                             Borrelia
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J databases.
                                                                               Length 193;
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Indels

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Gaps

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RESULT
Q9R7B2
AC
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Best Local S
Matches 180
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01-MAY-2000
01-JUN-2001
O98782 PRELIMINARY; PRT; 182 AA.
O98782; PRELIMINARY; PRT; 182 AA.
O198782; PRELIMINARY; PRT; 182 AA.
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update
OUTER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochaet).
Bacteria; Spirochaetales; Spirochaetaceae; Borre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; F
Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid cp26.
Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-2E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
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80; Conservative
                                                                                                                                                                                                                                                                                                                                            184
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200 AA;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
DE PROTEIN C PRECURSOR (FRAGMENT).
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Pred. No. 5.7e-35;
3; Mismatches 1
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Marti-Ras N., Postic D., Foretz M., Submitted (MAR-1997) to the EMBL/Ge EMBL, U91797; ABB81894.1; ... InterPro; IPR001800; Lipoprotein_6. pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ras N.M., Postic D., Foretz M., Bara "Borrelia burgdorferi sensu stricto, U.S.A.'?";
                                              InterPro; IPR001800; Lipoprotein_6
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1
                                                                                             Livey I., Gibbs C.P., Schuster R., "Evidence for lateral transfer and Lyme disease Borrelia.", Mol. Microbiol. 18:257-269(1995).
EMBL; L42895; AAB37003.1; -...
                                                                                                                                                                                                                                   Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel. 03, Created 01-MAY-1997 (TrEMBLrel. 03, Last see 01-JUN-2001 (TrEMBLrel. 17, Last an outer Surface PROTEIN C (FRAGMENT).
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                                                                                                                                                                                          STRAIN-28354;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      Borrelia burgdorferi (Lyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         VA 188
||
VA 182
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PD001149; Lipoprotein_6; 1.
193
193
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182 AA;
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nilarity 98.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
    AA;
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; 19202 MW;
    193
20411
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    MW;
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Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                Created)
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Pred. No. 1.2e-34;
l; Mismatches 1
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    05B68720F061E2A0 CRC64;
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icto, a bacterial
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                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updato)
01-JUN-2001 (TREMBLREL).
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NON_TER
SEQUENCE
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031122;
031122;
01-JAN-1998
01-JAN-1998
01-JUN-2001
  Bacteria; Spirochaetales;
NCBI_TaxID=139;
                    Plasmid cp26
Bacteria; Sp
                                                            Borrelia burgdorferi
                                                                                                                                                                                    Q9RQR8;
                                                                                                                                                                                                     Q9RQR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang I.-N., Dykhuizen D.E., Dunn J., Submitted (CCT-1997) to the EMBL/Ger EMBL, AF029871; AAB8654.1; InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1.
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01-JAN-1998 (TYEMBLrel. 05, Last sequence up
01-JUN-2001 (TYEMBLRel. 17, Last annotation
00TER SURFACE PROTEIN C (FRAGMENT).
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Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                   EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F01441; Lipoprotein_6; 1. PD001149; Lipoprotein_6; 1.
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nilarity 100.08;
Conservative 0
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194 AA;
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; 20640 MW;
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                    Spirochaetaceae; Borrelia
                                                            disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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EMBL/GenBank/DDBJ
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                                                            spirochete).
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Query Match
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Best Local S
Matches 180
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"Population dynamics of a naturally oc
Borrelia burgdorferi clones ";
Infect. Immun. 67:5709-5716(1999).
EMBL; AR074465; AAD23912.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
0TER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q44726 PRELIMINARY;
Q44726;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                 Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=297;
                                                                                                                                                                                                                                                                                                                                                                                          Borrella burgdorferi (Lyme disease spirochete)
Bacteria; Spirochaetales; Spirochaetaceae; Bor
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Plasmid.
NON_TER
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                              InterPro; IPR001800; Lipoprotein_6.
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                             259
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SEQUENCE FROM N.A.
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            IQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLE 318
IQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLE
                                                  NSGKGGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKK
                                                                   NSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKK 258
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Similarity 100.0%;
80; Conservative
                                                                                                                     Similarity
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                                                                                                                                                                            191 AA;
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201 AA;
                                                                                                          Conservative
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21457
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                                                                                                        Score 863; DB 2;
Pred. No. 1.3e-33;
0; Mismatches 1
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occurring heterogeneous
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immunoglobul
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01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
OUTER SURFACE PROTEIN C
                                                                                                                                                                  NCBI_TaxID=139;
MEDLINE-94075528: PubMed-8253951;
Theisen M., Frederiksen B., Lebech A.M., Vuust J.,
"Polymorphism in ospC gene of Borrelia burgdorferi
immunoreactivity of OspC protein: implications for
use of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation updat
0UTER SURFACE PROTEIN C (FRAGMENT).
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J. Bacteriol. 177:3036-3044(1995).
EMBL; X84783; CAA59254.1; -
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Best Local Similarity 97.6
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                                   "Evolution of the Borrelia burgdorferi
J. Bacteriol. 177;3036;3044(1995).
EMBL; X84779; CAA59250.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                  STRAIN=MUL;
MEDLINE=95286481; PubMed=7768799;
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STRAIN-TETS;
Marti-Ras N., Postic D., Foretz M., Baranton G.;
Marti-Ras N., Postic D., Foretz M., Baranton G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U91792; AAB81889.1;
EMBL; U91792; AAB81889.1;
InterPro; IPR001800; Lipoprotein_6.
InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.
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Bacteria; Spirochaetales; Spirochaetaceae; Borr
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                                                                                                                             Hansen K.;
                                                                                                                                     Theisen M., Borre M.,
                                                                                                                                                                                                        Bacteria; Spirochaetales;
NCBI_TaxID=139;
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MEDLINE-97478003; PubMed-9336916;

Ras N.M., Postic D., Foretz M., Baranton G.;

"Borrelia burgdorferi sensu stricto, a bacterial species 'made in U.S.A.'?";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (PRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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Search completed: March 18, 2002, 10:10:54 Job time: 977 sec THIS PAGE BLANK (USPTO)

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ALIGNMENTS

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AAB62715 standard; Protein;

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Chimeric - Borrelia sp. Chimeric - Borrelia sp.
        Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                      WPI; 2001-050113/06.
N-PSDB; AAF29019.
                                                                                                                         18-JUN-1999;
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                                                   (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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Best Local Similarity 99.7
...* 369; Conservative
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Chimeric -
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                                                                                                          Borrelia sp chimeric ospC
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                                                                                                                                                              AAB62716 standard; Protein;
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                                                                                         ospC; Lyme disease; vaccine; chimeric protein;
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Borrelia
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Best Local Similarity
Matches 323; Conserv
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87.5%; Pred. No. 2.2e-89;
Live 20; Mismatches 25; ?
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                                                                               352
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 43; Page 83-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compositions of OspC p
Lyme disease are used
to Lyme disease -
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(BROO-)
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Chimeric - Borrelia
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                                                        KNLSKAAKEMLINSVKELTS 371
                                                                                            kaeiekakkcseeftaklkgehtdlgkegvtddnakkailktnndktkgadeleklfesv
                                                                                                     KABIBKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESV
                                                                                                                                             EVETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGEL
                                                                                                                                   {\tt evetlltsidelakaigkkikndvsldneadhngslisgaylisnlitkkisaikdsgel}
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                                                                                                                                                                                                                  nklkekhtdlgkegvtdadakeailkangt-ktkgaeelgklfesvevlskaakemlans
                                                                                                                                                                                                                               TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKENLANS
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         standard;
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d to immunize animals and detect immune responses
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Pred. No. 9.5e
l0; Mismatches
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les 31;
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Lyme disease are used
to Lyme disease -
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Chimeric -
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                                                                                                                                                                                            Lyme
                     EKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLS
                                                KELTSPVVHG-----NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVET
                                                                                                                                  KLKDNHAQUGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV 180
                                                                                                                                                         present invention provides
KAAKEMLTNSVKELTS
              \tt ekakkcseeftaklkgehtdlgkegvtddnakkailktnndktkgadeleklfesvknls
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                                                                                                                      \verb|klkekhtdlgkegvtdadakeailktngt-ktkgaeelgklfesvevlskaakemlansv|
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)B; AAF29014.
                                                                                                                                                                                                                                    31 Similarity
327; Conser
                                                                                                                                                                                                                                                                                                 disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ospC; Lyme disease;
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Borrelia
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Pred. No. 1.8e-87;
9; Mismatches 32;
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These may be
be used as
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                                                                                                                                                                                                                                Sequence
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                EKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLS
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Borrelia
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Pred. No. 2.9e-87;
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N-PSDB;
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Lyme disease are used
to Lyme disease -
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(BROO-) BROOK
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                                                                                                                                                                                                                                                                                                                                                          Sequence
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DB; AAF29022.
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Pred. No. 5.3e-85;
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Query Match 82.3
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                                               Sequence
                                                                vaccines against Borrelia infection, to Lyme disease.
                                                                                                                Claim 43; Page 114-115; 160pp; English.
                                                                                                                                        Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                                                      to Lyme
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Pred. No. 5.8e-85;
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                                                      The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
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Lyme disease are used to immunize 
to Lyme disease .
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DB; AAF29018.
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Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                   INC.
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                                                                                                and
be
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Query

Match

82

.28

Score 1487.5;

DB

22;

Length

369;

The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi. B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea

leads

and

as leads

vaccines to Lyme d

disease.

Sequence

369

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RESULT 12
AAB62734
ID AAB627
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Chimeric -
                                                                                                                                                       Compositions of OspC |
Lyme disease are used
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N-PSDB; AAF29038.
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                                                                                               Claim 43; Page 139-140;
                                                                                                                                                                                                                                                                      Dattwyler RJ,
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(BROO-) BROOM
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                                 WPI; 200
N-PSDB;
    Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                                     Dattwyler RJ,
                                                                                        18-JUN-1999;
                                                                                                      19-JUN-2000; 2000WO-US16915
                                                                                                                                               Chimeric - Chimeric -
                                                                   (BROO-) BROOK
                                                                                                                    28-DEC-2000
                                                                                                                                  WO200078966-A1
                                                                                                                                                                   Borrelia; ospC; Lyme disease;
                                                                                                                                                                                Borrelia sp chimeric ospC protein SEQ ID
                                                                                                                                                                                                 03-APR-2001
                                                                         (UYNY ) UNIV NEW YORK STATE RES FOUND.
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                                 2001-050113/06.
DB; AAF29036.
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Borrelia
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                                                                  BIOTECHNOLOGIES
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                                                   Dykhuizen D,
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                                                                  INC.
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Pred. No. 8.7e-85;
'. Mismatches 31;
                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                           A
                                                                                                                                                                  chimeric protein;
                                                                                                                                                                                 NO:
                                                   Luft BJ,
                                                                                                                                                                                 83
                                                   Gomes-Solecki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                  Borrelia;
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; INFORMATIO		Sequence 11, Appl	US-09-196-293-11	4	212
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US-08-144-121-4	PCT-US93-07261-16	PCT-US93-07261-11	US-08-477-451-2	US-08-687-956A-23	US-08-466-662-5	US-08-471-491-5	US-08-470-260-5	US-08-894-017-23	US-08-446-137B-2	US-09-141-047-8	US-08-125-077-4	US-08-460-309-4	US-08-973-462-8	US-08-235-836C-116	US-08-235-836C-120	US-08-235-836C-114	US-08-235-836C-118
Sequence 4, Appl	Sequence 16, App	Sequence 11, App	Sequence 2, Appl	Sequence 23, App.	Sequence 5, Appl	Sequence 5, Appl	Sequence 5, Appl	Sequence 23, App	Sequence 2, Appl	Sequence 8, Appl	Sequence 4, Appl	Sequence 4, Appl	Sequence 8, Appli	Sequence 116, Ap	Sequence 120, Ap	Sequence 114, App	sequence iis, Ap

ALIGNMENTS

US-08-235-836C-107

RESULT

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-836C-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                      Ξ
                                                                                     E CHARACTERISTICS:
                                                                                                     AX: (516) 282-3729
ON FOR SEQ ID NO:
                                                                                                                                        MUNICATION INFORMATION:
HONE: (516) 282-7338
                                                                                                                                                                                           Bogosian, Margaret C. TRATION NUMBER: 25,324
                                                                                                                                                                                                                            IG DATE: 01-11-93
Y/AGENT INFORMATION:
                                                                                                                                                                                                                                                CATION NUMBER: US 08/148,191 
IG DATE: 01-11-93
                                                                                                                                                                                                                                                                                                               CATION NUMBER: US/08/235,836C
IG DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                      TING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         R READABLE FORM:
                                                                                                                                                                                                                                                                                PPLICATION DATA:
                                                                                                                                                                                                                                                                                                    IFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RY: USA
11973
                                                                                                                                                                                                                                                                                                                                                     APPLICATION DATA:
                                                 amino acid
                                                                     466 amino acids
                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                           25,324
                                                                                                                                                                            BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
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Query Match
Best Local Similarity
Matches 173; Conserv

Conservative

54;

Mismatches 119;

Indels

18;

38.8%;

Score 702; DB 4; Length 466; Pred. No. 2.2e-43;

15;

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INFORMATION FOR SEQ ID NO: 122

SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: amino acids
TYPE: alinear
; MOLECULE TYPE: US-08-235-836C-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-235-836C-122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 122, Application US/03235836C Patent No. 6248562
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGATEL C.
REGISTRATION UMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-11-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING STEERING Release **.., CURRENT APPLICATION DATA:

USCON CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NV
                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 ELTS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 GKKIHONNGLDTEYNHNGSLLAGRYAISTLIKOKLDGLKNEG-LKEKIDAAKKCSETFTN 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 MANNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 HGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDEL-AKAI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WNDSTSTLTISADSKKTKDLVFLTDGTITVQQYNTAGTSLEGSASEI--KNLSELKNALK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVIKGYVLEGTLTAEKTTLVVKEGTVTLSKNISK----SGEVSVELNDTDSSAATKKTAA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLLAGAYTISTLITOKLSKL--NGSEGLKEKIAAAKKCSEEFSTKLKDNHAQLGIQGVTD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                              (516) 282
(516) 282-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brookhaven National Laboratory
                                                                                                                                                                                                                         282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/148,191
                                                                                                                                                                    122:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #1.25
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US-08-235-836C-110
                   TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 01-11-93
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                       REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.8%;
Best Local Similarity 46.3%;
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patenth Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: Upton
CTTATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
   LENGTH:
                                                                                                                              NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 29-API
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 AEELGKLFESVEVLSKAAKEMLANSVKELTS 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 ADELEKLFESVKNLSKAAKEMLTNSVKELTS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 ESNAVVLAVKEVETLLTSIDEL-AKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 ASEIKNLSE-----LKNALK--GHPM--GNNSGKDGNTSANSADESVKGPNLTEISKKIT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 SGSLESLSKAAKEMLANSVKELTSPVVHGNNSGKDGNTSANSADESVKGPNLTEISKKIT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 CSEEFSTKLKDNHAOLGIQGVTDENAKK------AILKANAAGKDKGVEELEKL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 SSKVTKKQGSITEETLKANKLD--SKKLTRSNGTTLEYSQI----TDADNATKAV-ETLK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 NDGSLDNEANRNESLLAGAYTI-----STLITQKLSK-----LNGSEGLKEKIAAAKK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLDGLKNEG-LKEKIDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSIKLEG-----SLVVGKTTVEIKEGTVTLKREIEKDGKVKVFLNDTAGSNKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAIGKKIK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10, Application US/08235836C 6248562
466 amino acids
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                                                                                                                                                                                                                                                            29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                            US/08/235,836C
                                                                                                                                                                                                     US 08/148,191
                                     110:
                                                                                                            BNL93-28A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 701; DB 4;
Pred. No. 3.4e-43;
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TOPOLOGY: 1: ; MOLECULE TYPE: US-08-235-836C-110

Query Match Best Local Similarity

Score 692; DB 4; Pred. No. 1.1e-42;

Length 466

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TITLE OF INVENTION: ACTIVE proteins from Borrelia TITLE OF INVENTION: burgdorferi FILE REFERNCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER FILING DATE: 1998-03-10
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1992-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1989-12-22
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FOSTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 209
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US-09-196-293-15
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                                                                 ; ORGANISM: Borrelia
US-09-196-293-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKELTSPVVAESPKKPKQNVSSLDEKNSVSVDLPGEMKVLVSKEKNKDGKYDLIATVDKL
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                                                                                   burgdorferi
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36.48;
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Score 658.5;
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DВ
Length 209;
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US-08-158-353-3
, Sequence 3, Application US/08158353
; Patent NO. 5620862
; GENERAL INFORMATION:
; APPLICANT: Padula, Steven J.
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                                                                                                                        Matches
                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Carroll, Alice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS
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                                                         77 IGKKIHONNGLDTENNHNGSLLAGAYAISTLIKOKLDGLK-NEGLKEKIDAAKKCSETFT 135
                            60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
                                                                                                                                                                                                                                 TOPOLOGY: li
                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Hamilton, Brook, STREET: Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                        145;
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Disease
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                                                                                                                                                                                                                                                                                                                                                                                    33,542
                                                                                                                   Score 658.5; DB 1;
Pred. No. 1.1e-40;
""smatches 30;
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11; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                        UCT93-05
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                                                                                                                                                   Length 210;
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195 VKELTSPVV 203

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-836C-30
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                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BOOSIAN, MARGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPHONE: (516) 282-3729
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30,
Patent No. 6
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                                                  136 NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS 194
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
                             180 VKELTSPVV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                120
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                                                                                                                                77
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                      60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEEFS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 11bm. COMPUTER: 11bm. COMPUTER: PC-DOS/NO COMPUTER: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS 194
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                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Upton STATE: NY
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                                                                      TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS.179
                                                                                                                  IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKOKLDGLK-NEGLKEKIDAAKKCSETFT 135
                                                                                                                                                                                                                                                              144;
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amino acid
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                                                                                                                                                                                                                                                                        36.1%; 76.2%;
                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                     Score 653.5; DB 4;
Pred. No. 2.5e-40;
.1; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                    DB 4; Length 210;
                                                                                                                                                                                                                                                       Indels
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; Sequence 15, Application US/08209603E
; Patent No. 6248538
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RESULT 8
US-08-209-603E-15
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US-08-235-836C-36
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146
FILING DATE: 01-11-93
FILING DATE: 11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/08235836C Patent No. 6248562
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                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 207 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836
FILING DATE: 29-APR-1994
                                                                    193 KELTNPVV 200
                                                                                                   181 KELTSPVV 188
                                                                                                                             121 KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV 180
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CITY: Upton
cmare: NY
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APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                              61 GKKIKNDGSLDNEANRNESLLAGAYTISTLITOKLSKLNGSEGLKEKIAAAKKCSEEFST 120
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COUNTRY:
                                                                                                                                                                                                                                                                                  1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAI 60
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                                                                                                                                                                                              ISCNNSG--GDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAI 74
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (516) 282-7338
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                                                                                                                                                                                                                                                                                                                                               36.0%; Score 652; DB 4; 74.5%; Pred. No. 3.1e-40;
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Best Local S
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TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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DESCRIPTION: P
HYPOTHETICAL: N/
ANTI-SENSE: N/A
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENT
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORIGINAL S. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/EP90/0228: FILING DATE: 21-DEC-1990 APPLICATION NUMBER: US 07/862,535 FILING DATE: 19-JUN-1992 ATTORNEY/AGENT INFORMATION: NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                   POSITION IN GENOME:
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US/08/209,603E
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                                                                                                                                                                                                                                                                                                                                                                   MMEDIATE SOURCE:
LIBRARY: DSM 5662
136 NKLKEKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS
               120 TKLKDNHAQLGIQGYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS 179
                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ROBINSON, WILLIAM R. REGISTRATION NUMBER: 27,224 REFERENCE/DOCKET NUMBER: LK
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SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK
STATE: NY
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ZIP: 10016
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                                                                                              60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
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                                                              IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: BROOKS HAIDT HAFFNER & DELAHUNTY
99 PARK AVENUE
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                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N/A
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                                                                                                                                                                                                 36.0%; Score 651.5; DB 4; 76.2%; Pred. No. 3.4e-40; tive 11; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                   N/A
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                                                                                                                                                                                                                                                                                                  amino acid analysis
N/A
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US-08-031-295-2 ; Sequence 2, Application US/08031295 ; Patent No. 5530103

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                                                                                                                                                                                                                                                                       Query Match 33.0%; Score 597.5; DB 1; Best Local Similarity 69.1%; Pred. No. 2.8e-36; Constitute 20; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Padula, TITLE OF INVENTION: TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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195 VKELTSPVV 203
                 178 NSVKELTSPVVHGN 191
                                                                 136 DKLKSSHAELGIANGAATDANAKAAILKTNGT-KDKGAQELEKLFESVKNLSKAAQETLN 194
                                                                                       120 TKLKDNHAQLGIQ--GYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLA 177
195 NSVKELTSPVVAEN 208
                                                                                                                                                                                                     77
                                                                                                                                                       60 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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ZIP: 02173
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CITY: Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                   IGNLIAQNG-LNAGANQNGSLLAGAYVISTLIAEKLDGLKNSEELKEKIEDAKKCNKAFT 135
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linear
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Methods for Diagnosing Early Lyme
Disease
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                                                                                                                                                                                                                                                                                                       Length 212;
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RESULT 11
US-07-903-580-2
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GENERAL,
                                                                                                                                                                                                                                                                                                                                                                                     est Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 11-JUL-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,580
FILING DATE: 25-JUN-1992
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TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                       249
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                                                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 199303 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: July . . . CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 68.9 es 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                             LTS 202
                                                                                                                                                                                                                                                       KKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAK 308
                                                                                                                                           LTS 371
                                                                                                                                                                                                     LKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKE 368
                                                                                                                                                                         LAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANSVKE 199
                                                                                                                                                                                                                                      KKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDFTKK 139
   INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
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11-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                 Score 588; DB 1; 1
Pred. No. 1.3e-35;
3; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                Length 212;
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; Sequence 4, Application (
; Patent No. 5620862
; GENERAL INFORMATION:
; APPLICANT: Padula, St
; TITLE OF INVENTION: N
; TITLE OF INVENTION: I
                                                                                                                          RESULT 12
US-08-158-353-4
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PILING DATE: 22-JAN-1392

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,245

FILING DATE: 11-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/131
REFERENCE/DOCKET NUMBER: 30472/131
TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
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Best Local Similarity 68.5
Matches 126; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 NNSGKDGNT-SANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLTSIDELA-KAIG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                  369 LTS 371
                                                                                                                                                                                                                                                                                                              309 LKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKE
                                                                                                                                                                                                                                                                                                                                                                                                                     249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                           LAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANSVKE
                                                                                                                                                                                                                                                                                                                                                                                              KKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAK 308
                                                                                                                                                                                                         LTS 202
                                                                                                                                                                                                                                                                                                                                                                        KKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDFTKK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATKAIG 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
               Steven J.
Methods for Diagnosing Early Lyme
                                                                                                         US/08158353
    Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 588; DB 4; 68.9%; Pred. No. 1.3e-35;
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive

Smith & Reynolds, P.C

STREET: Iwo

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US-08-235-836C-32

; Sequence 32, Application US/08235836C
; Patent No. 6248562
; Patent No. 6248562
; Patent No. 6248562
; Patent No. 6248562
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
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Best Local Similarity 67.2%; Pred. No. 2.8e-33;

19: Mismatches 39; Indels
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                         TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor NUMBER OF SEQUENCE: 144 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 617-861-6240
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                  200 LTS 202
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REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                   COUNTRY: UZIP: 11973
                                                 CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                        ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                        LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 139
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                                    USA
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CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: DE P39 42 728.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09196293 Patent No. 6183755 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fuchs, Renate
APPLICANY: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANY: Wilske, Bettina
APPLICANY: Preac-Mursic, Vera
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Active proteins from Borrelia TITLE OF INVENTION: burgdorferi FILE REFERENCE: 738.001US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: BN TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TKLKDNHAQLGIQGYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ISCNNSG--GDTASTNPDESAKGPNLTVISKKITDSNAFVLAVKEVEALISSIDELANKA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 64.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 29-APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELA-KA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGKVIHQNNGLNANAGQNGSLLAGAYAISTLITEKLSKLKNSEELNKKIEEAKNHSEAFT
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APPLICATION UNMER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 17.224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELEPHONE: (212) 697-3355
TELEPHONE: (212) 697-3355
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US-08-209-603E-11
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US-09-196-293-11
                TELEFAX: (212) 557-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08209603E Patent No. 6248538
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LENGTH: 212
TYPE: PRT
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                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,603E
FILING DATE: 10-MAR-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: ATST - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-MURSIC, VERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 10016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 LKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKE 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 KKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEFTAK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 NNSGKVGILTSTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG 79
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Search completed: March 18, 2002, 09:55:34 Job time: 347 sec

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                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
                                  FRAGMENT TYPE: 1
ORIGINAL SOURCE:
200 LTS 202
                     369 LTS 371
                                                309 LKGEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESYKNLSKAAKEMLTNSVKE 368
                                                                              IMMEDIATE SOURCE:
LIBRARY: DSM 5662
POSITION IN GENOME:
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AMINO ACID
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Gaps

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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DB seq length: 2000000000
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1809
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                   /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US090_COMB.pep:*
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165.825 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length DB	DB	ID	Description	
_	1809	100.0	371	19	US-09-596-746A-34		Appl
2	1804	99.7	370	19	US-09-596-746-34	34,	Appl
ω	1801	99.6	394	19	US-09-596-746-64	64,	Appl
4	1801	99.6	395	19	US-09-596-746A-64	64,	Appl
5	1564.5	86.5	370	19	US-09-596-746A-36	36,	Appl
0	1559.5	86.2	369	19	US-09-596-746-36	36,	Appl
7	1556.5	86.0	393	19	US-09-596-746-66	66,	Appl
80	1556.5	86.0	394	19	US-09-596-746A-66	66,	Appl
9	1534	84.8	375	19	US-09-596-746A-24	24,	App1

5	44	43	42	41	40	39	3 8	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	ŀ
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9-596-746-5	9-596-746A	-09-596-746-	9-596-746-	9-596-746A-5	9-596-746A	-96	-596-746-	9-596-746A-4	S-09-596-746A	-09-596-746-	-09-596-746A	-09-596-746-	9-596-746-	-09-596-7462	-09-596-746-3	S-09-596-746	-09-596-746A-7	-09-596-746-7	-09-596-746A-	-09-596-746-6	96-746A-	96-746-7	-09-596-	-09-596-746A-	-09-596-746-5	-09-596-746-4	-09-596-746A-	9-596-746A-4	-09-596-746A-8	9-596-746-8	9-596-746A-	-09-596-746-6	S-09-596-746-2	96-7	
equence	Sequence 78,	Ø	Ø	Ð	Ø	O	ø	æ	Ø	Ø	Ø	Ø	Ø	O	Ø	Ø	Ø	Ø	æ				Sequence 32,		æ			Φ	Ø	Φ	æ	Sequence 60,	Sequence 24,	ø	eduction
Appl	, Appl	, Appl	, Appl	Appl	Appl	, Appl	, Appl	Appl	App1	Appl	. Appl	Appl	, Appl	, Appl	. Appl	, Appl	, Appl	, Appl	, Appl	Appl	Appl	Appl	, Appl	. Appl	, Appl	Appl	. Appl	. Appl	, Appl	, Appl	, Appl	Appl	Appl	, Appl	1771

ALIGNMENTS

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; FEATURE:
; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-596-746A-34
                                                                                                                                                                   SOFTWARE: FastSEQ for Windows
SEQ ID NO 34
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity
Matches 371; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/09596746A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                        APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ. ID NOS: 84
                                                                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dattwyler, Raymond J.
Seinost, Gerald
    100.0%; Score 1809; DB 19; ilarity 100.0%; Pred. No. 1.9e-120; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          Cause Lyme Disease
      Indels
                                            Length 371;
      0;
                                                                                                                                                                                                                                                                                                                                                                                                               in Humans
    Gaps
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ORANISM: Artificial Sequence OTHER INFORMATION: OSPC Chimera Ouery Match Best Local Similarity 99.7%; Score 1804; DB 19; Length 370; OY 2 ACMNSGKDGMTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAIG 60; IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 2 US-09-596-746-34 Sequence 34, Application US/09596746 APPLICANT: Dattwyler, Raymond J. APPLICANT: Schootler, Raymond J. APPLICANT: Dykhuizen, Dailal TITLE OF INVENTION: Gorald CURRENT APPLICANT: Dyknuizen, Dailal FILE OF INVENTION: Goras-Solecki CURRENT APPLICATION: Bornelia borrelia burgdorferi and PRIOR APPLICATION: Goras-Solecki CURRENT APPLICATION: US-009-596-746 RESURENT APPLICATION: US-009-596-746 NUMBER OF SON NUMBER: US-00-06-16 NUMBER OF SON NUMBER: US-00-06-16 SONTHAR: PAD IN NUMBER: US-00-06-18 SONTHAR: SPAN NUMBER: US-00-06-18 TYPE: DB-00 T	OY OY OY ORKINDGSLDNEANNESSLAGAPTISTLTOKLSKLINGSBELKEKIAAKINGSLESKATOSNAVLLAVKEVEALLUSSIDELAKAI OP 1	Db Hilling
Duery Match Best Local 36 imilarity 99.6%; Score 1801; DB 19; Length 394; QY 2 ACNNSGRONTSANSADESVKGPNITEISKKITDSNAVLLAVKEVEALLSSIDELAKAIG 61 Db 25 SCNNSGRONTSANSADESVKGPNITEISKKITDSNAVLLAVKEVEALLSSIDELAKAIG 61 QY 62 KKIKNDGSLDNEANRNESLLAGAYTISTLITOKLISKNESEGLKEKIAAAKKGSEEFSTK 141 Db 16	Sequence 7.45-64 Sequence 64, Application US/09596746 APPLICANT: Dattwyler, Raymond J. APPLICANT: Dykhuizer, Darial TITLE OF INVENTION: Gerald APPLICANT: Luft, Benjamin J. TITLE OF INVENTION: Groups of Borrella burgdorferi and CURRENT APPLICATION Groups of Borrella burgdorferi and PRICA APPLICATION: BORDER: US/09/296,746 FURRENT EPILICATION BORDER: US/09/596,746 FURRENT APPLICATION BORDER: US/09/596,746 PRIOR APPLICATION WUMBER: US/09/596,746 SOFTMARE OF TO MUMBER: US/09/596,746 SOFTMARE OF TO MUMBER: US/09/596,746 SOFTMARE OF TO MUMBER: US/09/596,746 SOFTMARE APSLED MOS: 84 06-18 TIPE: PRT US-09-596-746-64 Chimera	us-09-596-74	

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                                                                                                                                                                             Sequence 36, Application US/09596746A
GENERAL INFORMATION:
APPLICANT: Dattryler, Raymond J.
APPLICANT: Seinost, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 64, Application US/09596746A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: 1099/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-66-18
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US 60/146A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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6 LTNSVKELTS 395
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                                                                             Cause Lyme Disease in
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; OTHER INFORMATION: OSPC Chimera US-09-596-746-36
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NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 36
LENGTH: 370
                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 36
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                             sequence 36, Application US/09596746 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                     APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                     LENGTH: 369
TYPE: PRT
ORGANISM: Artificial Sequence
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                                 FEATURE:
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Query Match

Score 1559.5;

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Length

87.5%;

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US-09-596-746-66
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US-09-596-746-66
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SEQ ID NO 66
LENGTH: 393
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Best Local :
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Matches
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
RIOR FILING DATE: 1999-06-18
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; ORGANISM: OSPC Chimera US-09-596-746A-66
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; SOFTWARE: FastSEQ
; SEQ ID NO 66
; LENGTH: 394
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Best Local Similarity
Matches 322; Conserv
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US/60/140,042
PRIOR FILING DATE: 1999-06-18
361 MLTNSVKEL 369
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                                                                                                           ELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKK 300
                                                                                                                                                                                       LKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSVK 181
                                                                                                                                                                                                                                                                       LKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSVK 205
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Pred. No. 2e-102;
Pred. No. 2e-102;
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US-09-596-746-28
Sequence 28, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
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US-09-596-746A-24
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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Best Local Similarity 87.0%;
Matches 328; Conservative 9
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SEQ ID NO 24
LENGTH: 375
TYPE: PRT
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APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D.
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                                                                                                                                                                                                                                            SKAAKEMLTNSVKELTS 375
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Pred. No. 7.
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7.5e-101;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Dises
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 1000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 199-06-18
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 28
                                                                                         NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Wi
SEQ ID NO 28
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Best Local
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                          TYPE: PRT ORGANISM: Artificial Sequence
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                                                                      LENGTH:
OTHER INFORMATION: OspC Chimera
                    FEATURE:
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                                                                                                            Windows
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                                                                                                          Version
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US-09-596-746A-28

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Query Match 84.8% Best Local Similarity 86.3% Matches 328; Conservative

84.8%; Score 1533.5; DB 19; 86.3%; Pred. No. 8.3e-101; tive 10; Mismatches 31; I

Length 378;

11;

Gaps

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APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki
FITLE OF INVENTION: Groups of Borrelia burgdorferi and
FITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea

CURRENT APPLICATION NUMBER: US/09/596,746

CURRENT FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 374
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US-09-596-746-24
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                                                                                                                       Query Match
Best Local 9
                                                                                                          Matches
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                                            NKLKEKHTDLGKEGVTDADAKEA.ILKANGT-KTKGAEELGKLFESVEVLSKAAKEMLANS
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                                                                                                         Conservative
                                                                                                                         84.5%;
87.0%;
                                                                                                         Score 1529; DB 19;
pred. No. 1.7e-100;
9; Mismatches 32;
                                                                                                                                         Length
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; GENERAL INFORMATION:
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LENGTH: 398
TYPE: PRT
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Groups of Borrelia burgdorferi TITLE OF INVENTION: Borrelia afzelii That Cause Lym FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                            Matches 326;
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APPLICANT:
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                                                                           KELTSPVVHG-----NNSCKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVET
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                         GKKIKNDGSLDNEANRNESLLAGAYTISTLITOKLSKLNGSEGLKEKIAAAKKCSEEFST 120
                                                                                                                                 KLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSV 180
                                                                                                                                                                                     GKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIDAAKKCSETFTN 143
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Maria J.C. Gomes-Solecki
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Seinost, Gerald
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                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                               84.4%; Score 1526; DB 19;
86.7%; Pred. No. 3.1e-100;
htive 10; Mismatches 32;
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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 399
TYPE: PRT
ORGANISM: OSPC Chimera
US-09-596-746A-60
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US-09-596-746A-60
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GENERAL INFORMATION:
APPLICANT: Dattwyle
APPLICANT: Seinost,
APPLICANT: Dykhuize
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Best Local Similarity
Matches 326; Conserv
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APPLICANT:
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Maria J.C. Gomes-Solecki
Dattwyler, Raymond J.
Seinost, Gerald
Dykhuizen, Danial
                                                    Application US/09596746
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86.7%; Pred. No. 3.1e-100;
tive 10; Mismatches 32;
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; SOFTWARE: FastSI; SEQ ID NO 80; LENGTH: 401; TYPE: PRT; ORGANISM: OSPC (US-09-596-746-80)
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Best Local Similarity
Matches 326; Conserv
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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NLSKAAKEMLTNSVKELTS
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                                                                       AEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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86.0%; Pred. No. 4e-100;
tive 10; Mismatches 3
                                    371
 401
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Search completed: March 18, 2002, 10:08:45 Job time: 973 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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182.5
182.5
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1: /cgn2_6/ptcodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptcodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptcodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptcodata/2/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptcodata/2/paa/US10_NEW_COMB.pep:*
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Match
           303921 seqs, 63882009 residues
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US-09-978-427-15044

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US-09-815-242-5883

US-10-072-851-13080

US-10-072-851-15590

US-10-072-851-15590

US-10-072-851-15590

US-10-0708-427-19883

US-09-708-427-19883

US-09-708-427-19881

US-09-708-427-3731

US-09-708-427-3731

US-09-708-427-3739

US-09-614-150-10224

US-09-614-150-10231

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US-09-614-150-10231

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US-09-815-242-12996
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  Sequence
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7, Appli
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	PNLTEISKKITDSNAVL	i Score 886; DB 6; Pred. No. 5.9e-54; Mismatches 2	J J-derived peptide /09/974,992 10 80,089 DK97/00203	ALIGNMENTS	US-09-614-150-17349 US-10-032-585-7611 US-10-072-851-15555 US-09-815-242-581-824 US-09-614-150-4824 US-09-614-150-25386 US-09-614-150-25386 US-09-614-150-25386 US-09-614-150-25386 US-09-614-150-25386 US-09-614-150-6213 US-09-614-150-6213 US-09-614-150-6213 US-09-614-150-2610 US-09-815-242-12610 US-09-815-242-12688 US-10-072-851-12888 US-09-815-242-5803
	EALLSSIDELAKAI 6	Length 211; ; Indels 0; Gap	fragments		Sequence 1: Sequence 5: Sequence 5: Sequence 6: Sequence 4: Sequence 7: Sequence 7: Sequence 7: Sequence 7: Sequence 1: Sequence 5:
	96	ů			7344, Ap 5555, Ap 834, Ap 824, Ap 5386, A 6313, A 6313

RESULT 2 US-09-974-992-3

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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR APPLICATION NUMBER: PCT/DK97/00203
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 207
TYPE: PRT
ORGANISM: Borrelia garinii
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               Best Local Similarity Matches 123; Conserv
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PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
                                            Query Match
                                                                                             LENGTH: 212
TYPE: PRT
ORGANISM: Borrelia afzelii
-09-974-992-7
                                                                                                                                                                                                                                                                                                                                                                                                   requence 7, Application US/09974992
NERAL INFORMATION:
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                     APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 36.3%; Score 656; DB 6; Length 207; Best Local Similarity 75.0%; Pred. No. 3.8e-38; Matches 141; Conservative 20; Mismatches 23; Indels
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APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
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                         30.7%;
           19;
                      Score 556; DB 6;
Pred. No. 2.9e-31;
        Mismatches
                                   Length 212;
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LOCATION: 1..1304
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1304
OTHER INFORMATION: Ceres Seq. ID 1828628
US-09-708-427-15045
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243B
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15045
LENGTH: 1304
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Arabidopsis thaliana
301 CSEEFTAKLKGEHTDLGKEGYTDDNAKKAILKTNNDKTKGADELEKLFESYKNLSKAAKE
                                                 361 SIKSELEISQEEKTRALDNEKAATSN-----IQNLLDQRTELSIELERCKVEEEKSKK
                                                                                                                    301 KQLAELNHVLHETKSDNAAQKEKIELLEKTIEAQRTDLEEYGRQVCIAKEEASKLENLVE
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                                                                                                                                                                                                                                                                                                                                                            LLSSIDELAKAIGKKIKNDGSLDNEA-NRNESLLAGAYTISTLITQK-----LSKLNG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                 SLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKK 300
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23.4%;
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Pred. No. 7.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
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FEATURE: misc_feature
LOCATION: 1..1313
OTHER INFORMATION: Xaa is a
NAME/KEY: misc_feature
LOCATION: 1..1313
OTHER INFORMATION: Ceres Se
US-09-708-427-15044
RESULT 6
US-09-815-242-5883
; Sequence 5883, Application US/09815242
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15044
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Best Local Similarity
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                  ----MLTNSVKELTS
                                                                                                                                                                                 DMESLTLAL-----QEASTESSEAKATLLVCQEELKNC---ESQVDSLKLASKETNE
                                                                                                                                                                                                                      CSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKE
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                                                                                                                                                                                                                                                                                ------SLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKK 300
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Pred. No. 7.
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7.3e-05;
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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SEQ ID NO 5883
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
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                               QHAKDEATALINSSNDLNQAQKDALKQQVQNATT
                                                                TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 371
                                                                                                                                                                                 ASQSLGSLDNLNNAQKQTVTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATK 622
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                                                                                                                                          AEI-----EKAKK-------CSEEFTAKLKGEHTDLG--KEGVTDDNAKKAILKTNNDK 337
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Zyskind, Judith W.
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Yamamoto, Robert T.
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Trawick, John D.
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Pred. No. 4.4e-05;
2; Mismatches 183;
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Best Local Similarity
Matches 101; Conser
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LENCTH: 837
TYPE: PRT
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                                  TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 371
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QHAKDEATALINSSNDLNQAQKDALKQQVQNATT 716
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Yamamoto, Robert T
Roemer, Terry
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Zyskind, Judith W.
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Zamudio, Carlos
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Pred. No. 4.4e-05;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13080
LENGTH: 875
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Best Local :
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-02-16
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338 TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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                                                                                                                                                                                VETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELK 292
                                                                                                                                                                                                                                                                                                                                                                                                                   S--EEFSTKLKD-NHAQLGIQ-GVTDENAKKAILKANAAGKDKGVEELEKLS------G 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDG-----SLDNEANRNESLLAGAYTISTLITQKLSKLNGS--EGLKEKIAAAKKC 114
                                                                                                AEI----EKAKK-----CSEEFTAKLKGEHTDLG--KEGVTDDNAKKAILKTNNDK 337
                                                                                                                                           ASQSLGSLDNLNNAQKQTYTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATK
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Xu, H. Howard
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Pred. No. 4.6e-05;
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Best Local Similarity
Matches 101; Conserv
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13080
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                       QHAKDEATALINSSNDLNQAQKDALKQQVQNATT 753
                                                                                                                                                                                       ASQSLGSLDNLNNAQKQTVTDQINGAHTVDEANQIKQNAQNLNTAMGNLKQAIADKDATK
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                                                            TKGADELEKLFESVKNLSKAAKEMLTNSVKELTS 371
                                                                                                                                            AEI-----EKAKK-------CSEEFTAKLKGEHTDLG--KEGVTDDNAKKAILKTNNDK
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Yamamoto, Robert T
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Zyskind, Judith W.
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Zamudio, Carlos
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; Pred. No. 4.6e-05;
62; Mismatches 183
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US-10-032-585-7646
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; GENERAL INFORMATION:
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SEQ ID NO 7646
LENGTH: 1881
TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                        Sequence 15590, Application US/10072851 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 101; Conserv
                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Terry, Roemer D
                                                                                  APPLICANT:
                                                                                                   APPLICANT: Carr,
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  APPLICANT:
                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITKKISAIKDSGELKA-----EIEKAK------KCSEEFTAKLKGEHTDLGK-- 318
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                                                                                                                                                                                                                                                                                        KLFESVKNLSKAAKEMLTNSVKELTS
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                                                                                                                                                                                                                                                                                                                                                                        EGVTD------DNAKKAILKTNNDKTKGADELE-----
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                                    Foulkes, J. Gordon
Zamudio, Carlos
Ohlsen, Kari L.
                                                                                  Xu, H. Howard
                       Haselbeck, Robert
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                                                                                                       Grant J.
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RESULT 12
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; NAME/KEY: MISC_FEATURE
; LOCATION: (1881)..(1881)
; OTHER INFORMATION: X-any amino acid
US-10-072-851-15590
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      Sequence 19883, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 101;
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TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITAR, 028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
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APPLICANT:
APPLICANT:
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EQ ID NO 15590
LENGTH: 1881
TYPE: PRT
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NUMBER OF SEQ ID NOS: 15811
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                                                                                                                                                                                                                                                                                                                                                                                                                      DALKQSQKEYKTLKTKNSDTESKLEKQLEELEKVKSDLQTADE-KLKGITEREIALKSEL 1715
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Boone, Charles
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Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; Score 182.5; DB 7 22.6%; Pred. No. 0.00026;
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                            AND CORRESPONDING
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                          POLYPEPTIDES
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US-09-708-427-19882

Sequence 19882, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.
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; NAME/KEY: misc_feature
; LOCATION: 1..1014
; OTHER INFORMATION: Ceres Seq. ID 1836847
US-09-708-427-19883
                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 19882
LENGTH: 1018
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1983
LENGTH: 1014
TYPE: PRT
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Best Local
NAME/KEY: misc_feature
LOCATION: 1..1018
OTHER INFORMATION: Xaa is any amino
NAME/KEY: misc_feature
LOCATION: 1..1018
                                                                                                   ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 GAKCQGLEKESGDLAEVNLKLNLELANHGS-----EANELQTKLSALEAEKEQTANEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 NDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTKLKDN 125
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NAME/KEY: misc_feature
LOCATION: 1..1269
OTHER INFORMATION: Xaa is al
NAME/KEY: misc_feature
LOCATION: 1..1269
OTHER INFORMATION: Ceres See
US-09-708-427-19881
                                                                                                                                                                                                                                                                                                                               US-09-708-427-19881
US-09-708-427-19881, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
EQ ID NO 19881
LENGTH: 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520 SAEESLEQKGREIDEATTKRMELEALHQSLSIDSEHRLQKAMEEFTSRDSEASSLTEKLR 579
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NDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTKLKDN 125
                                                                            SADESY--KGPNLTEISKKITDSNAY--LLAVKEVEALLSSIDEL-----AKAIGKKIK 65
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Similarity 24.4%;
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1101 QLKENVENAATASVKVAELTS
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                                                                 353 NLSKAAKEMLTNSVK--ELTS
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                                                                                                                               EASKTTIEDLTKQLTSEGEKLQSQIEKLRAVAAEKSVLESH-----FEELEKTLSEVKA 1100
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; LOCATION: 1..1144
; OTHER INFORMATION: Xaa is
; NAME/KEY: misc_feature
; LOCATION: 1..1144
; OTHER INFORMATION: Ceres S
US-09-708-427-15046
                                                                                                                                                                                                                                                                                                                                                          Sequence 15046, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 15046
LENGTH: 1144
                                                                                                                                                         TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                    NAME/KEY: misc_feature
                                                                                          15
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Query Match

Conservative

42;

Mismatches 154;

Indels Length 1144;

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Gaps

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9.48;

Score 169.5; DB Pred. No. 0.0011;

DB 6;

606 NLVDNVANMQNIAEESKDLRE-----REV-AYLKKIDELSTANGTLADNVTNLQNIS

15 NSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAIGKKIKNDGSLDNEA 74

657 EENKELRERETTLLKKAEELSELNESLVDKASKLQTVVQENEELRERETAYLKKIEELSK

716

75 NRNE-----SLLAGAYTISTL---ITQKLSKL----NGSEGLKEKIAAAKKCSEEFST 120

819

233 VETLLTSIDELAKAIGKKIKNDVSLDNEADHNGSLISGAYL----ISNLITKKISAIKDS

NKENELHGMVVEIEDL-RSKDSLAQKKIEELSNFNASLLIKE-NELQAVVCENEELKSKQ

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NSVKELTSPVVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVV-----LAVKE

VSTLKT-IDELSDLKQSLIHKEKELQAAIVENEKLKAEAALSLQRIEELTNLKQTLIDKQ

877 288 717

LHEILSDQETKLQI-----SNHEKEELKERETAYLKKIEELSKV------

-QEDLL 760

K----LKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLA 177

Search completed: March 18, 2002, 09:58:23 Job time: 381 sec

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Result
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Copyright (c) 1993 - 2000
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410.946 Million cell updates/sec
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A; Status: nucleic acid sequence not shown

Lyme di

outer surface protein C - Lyme disease sp C;Species: Borrelia burgdorferi (Lyme dis C;Date: 12-Feb-1998 #sequence_revision 20 C;Accession: S70280 R:Livey, I.; Gibbs, C.P.; Schuster, R.; D Mol. Microbiol. 18, 257-269, 1995 Mol. Microbiol. 18, 257-269, 1995 A;Reference number: S70255; MUID:96296448 A;Accession: S70280	RESULT		45	44	43	42			39			36	35	34	33	32	31	30	
rface page Borre Borre 12-Feb-1 Ion: S7(I.; Git robiol. Evidence numble ion: S7(1		588	589.5	590.5	592	595.5	597	599	602.5	603	605.5	606	607	607.5	808	608	609.5	
			32.5		•	32.7	2	33.0	33.1	ω	w	33.5	w	w	w	w	33.6	W	
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outer surface protein C - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Species: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000 C;Accession: S70280 C;Accession: 1: Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 A;Reference number: S70255; MUID:96296448 A;Recession: S70280		ALIGNMENTS	140142	S70289	869916	140281	569932	S70278	140273	S54197	140104	S70274	140125	S70268	140129	140279	869923	\$70273	
change in OspC			outer	outer	outer	outer	outer	outer	outer	outer	outer	outer	outer	outer	outer	outer	outer	outer	
26-May-2000 variation in					surface prot		surface prot	surface prot						surface prot					
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A; blatus. ......
A; Molecule type: DNA
A; Residues: 1-193 <LIV>
A; Cross-references: EMBL:L42868; NID:g858735; PIDN:AAB37011.1; PID:g1695226
A; Cross-imental source: strain ZS7
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                                                                                                                                                                                                                                  C;Genetics:
A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
                  Qy
В
                                                                                                                                                                                Matches 183;
                                                                                                                                                                                          Query Match
Best Local Similarity
183 LTSPVV
||||||
181 LTSPVV
                                           121 KDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSVKE
                                                                  123
                                                                                       KDNHAQLGIQGYTDENAKKAILKANAAGKDKGYEELEKLSGSLESLSKAAKEMLANSYKE
                     188
 186
                                                                                                                                                                                Conservative
                                                                                                                                                                                         48.98;
                                                                                                                                                                             Score 884; DB 2; L
Pred. No. 2.9e-34;
Pred. No. 2.9e-34;
                                                                                                                                                                                                     Length 193;
                                                                                                                                                                                 Indels
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                                                                                                                                                                                Gaps
                                              180
                                                                                                                                    60
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outer surface protein C precursor - Lyme disease spirochete (strain PBre) C; Species: Borrella burgdorferi (Lyme disease spirochete) A; Variety: strain PBre A; Variety: strain PBre C; Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-200 C; Accession: S69918; 572674; I40103 R; Jauris-Heipke, S; Liegl, G; Preac-Mursic, V.; Roessler, D.; Schwab, E J. Clin. Microbiol. 33, 1860-1865, 1995 J. Clin. Microbiol. 33, 1860-1865, 1995 A; Title: Molecular analysis of genes encoding outer surface protein C (Os)

encoding outer surface protein C (OspC) of Borre

D.; Schwab, E.; Soutschek 26-May-2000

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A;Gene:
C;Superf
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A;Molecule type: DNA
A;Residues: 1-210 <RES>
A;Cross-references: EMBL:U04281; NID:9434663; PIDN:AAC43297.1; PID:9434664
R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
MOI. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448
                                                                                                                                                A;Cross-references: EMBL:L42893; NID:g858721; A;Experimental source: strain 297
                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 19-210 <LIV>
                                                                                                                                                                                                                   A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer surface protein C precursor - Lyme disease spirochete C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_chec.
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I40144
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A;Accession: S69918
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-211 <JAU>
A;Cross-references: EMBL:X81522; NID:9872021; PIDN:CAA57242.1; PID:9872022
A;Experimental source: strain PBre
R;Roessler, D.
Submitted to the EMBL Data Library, September 1994
A;Reference number: S72674
A;Accession: S72674
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Query Match
Best Local Similarity 99.4
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A:Residues: 1-152, 'E', 154-211 <RC
A:Cross-references: EMBL:X81522;
                                                                                                                                     Genetics:
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Title: Expression and sequence of outer surface Reference number: I40143; MUID:95154673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KELTSPVV 188
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99.4%;
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22: NID:g872021; PIDN:CAA57242.1;
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              0
         Pred. No. 5.300; Mismatches
                            Score 879;
Pred. No. 5.
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Pred. No. 3.5e-34;
4; Mismatches 2
                                             DB 2;
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                                         Length 210;
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Outer surface protein C - Lyme disease spirochete (strain HUR) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-200 C;Accession: I40106; S54185 R;Pheisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Haritle: Evolution of the Borrelia burgdorferi outer surface protein Ospc. A;Reference number: I40104; MUID:95286481 A;Status: preliminary; translated from GB/EMBL/DDBJ. A;Molecule type: DNA A;Residues: I-178 <RES>
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C;Superfamily:
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A; Residues: 1-203 < RES>
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A; Title: Polymorphism in
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R; Theisen, M.;
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                                                                                                                                                                                                                                                                                                                     KELTSPV 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cal Similarity
179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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95.78;
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Pred. No. 3.1e-33;
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                                                                                                                    Lebech, A.M.; Hansen,
                                                                                                                                                   26-May-2000
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A;Cross-references: E
C;Genetics:
A;Gene: ospC
C;Superfamily: Lyme c
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A;Variety: strain PKa
C;Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
C;Accession: S69927; S72669
R;Jauris-Heipke, S; Liegl, G; Preac-Mursic, V; Roessler, D; Schwab, E; J
J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC)
A;Reference number: 140047; MUID:95395018
A;Accession: S69927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A; Reference number: S72669 A; Accession: S72669
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A; Residues: 1-124,'D',126-139,'E'
A; Cross-references: EMBL:X69589
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A; Residues: 1-210 < JAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer surface protein C precursor - Lyme disease spirochete (strain C;Species: Borrelia burgdorferi (Lyme disease spirochete)
В
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Best Local Similarity
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Best Local
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                                                                                       TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS 179
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VKELTSPVV 203
                                                                                                                                                            IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS 119
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                                   VKELTSPVV 188
                                                                    NKLKDKHTDLGKEGVTDADAKEAILKTNGT-KTKGAEELGKLFESVEVLSKAAKEMLANS
                                                                                                                                         IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLK-NEGLKEKIEAAKKCSETFT
                                                                                                                                                                                                                                                                                      146;
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                                                                                                                                                                                                                                                                                               36.78;
77.28;
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Pred. No. le-32;
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Pred. No. 3.8e-24;
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outer surface protein C - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 13:Feb-1998 #sequence_revision 13:Feb-1998 #text_change 21-Jul-2000 C;Accession: G70218; 140269; S37726; S70281
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                          Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease
A; Reference number: A70100; MUID:98065943
A; Accession: G70218
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C;Superfamily: Lyme disease spirochete surface
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                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-210 <RES>
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A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Med. Microbiol. Immunol. 182, 37-50, 1993
                                                                                                                                      R;Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence
A;Reference number: 140269; MUID:96025162
A;Accession: 140269
                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000792; NID:g3253098; A;Experimental source: strain B31
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A;Experimental source: strain 28354
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A; Residues: 1-193 <LIV>
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                                                                                                                                                                                                                                                                                                           A;Mòlecule type: DNA
A;Residues: 1-210 <KLE>
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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKK
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Pred. No. 4.1e-24;
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                          ; PID:g769684
Schwab, E.;
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Genetic heterogenity of the genes coding for the outer surface

protein C Soutschek,

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C;Superfamily: Lyme disease spirochete surface protein
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I40122
                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X73626; C;Genetics:
                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-200 < RES>
                                                                                                                                                                                                                                                                                                                                                                       R;Theisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J.; Ha
J. Clin. Microbiol. 31, 2570-2576; 1993
A;Title: Polymorphism in ospC gene of Borrelia burgdorferi
A;Reference number: I40105; MUID:94075528
                                                                                                                                                                                                                                                                                                                                                                                                                                        outer surface protein C - Lyme disease spirochete (strain DK6) (fragment) Cispecies: Borrelia burgdorferi (Lyme disease spirochete) te: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-20 ccession: I40122; S34177
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A;Accession: S37726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <JAU>
A;Cross references: EMBL:X69596; NID:g311391; PIDN:CAA49306.1; PID:g311392
R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation
                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
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A;Residues: 19-210 <LIV>
A;Cross-references: EMBL:L42887; NID:g858715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Reference number: S70255; MUID:96296448
A:Accession: S70281
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Best Local Similarity
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                 GKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLN-SEELKEKIKEAKDCSEKFTT
                                                                                                  MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELAKAI 60
                                                 GKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFST 120
                                                                                ISCNNSG--GDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKELTSPVV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS
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                                                                                                                                                                    Similarity
                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid sequence not shown
                                                                                                                                                                 36.3%;
75.0%;
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76.7%; Pred.
                                                                                                                                                                                                                                                                                     NID: g313277; PIDN: CAA52005.1;
                                                                                                                                                   Score 656; DB 2
Pred. No. 8e-24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                       from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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No. 6.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN: AAB36995.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                    2
                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                                                                        and
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                                                                                                                                                                                                                                                                                      PID:g313278
                                                                                                                                                                                                                                                                                                                                                                                       immunoreactivity
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S69919
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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Do
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and
A;Reference number: S70255; MUID:96296448
A; Experimental source: C; Genetics:
                                                         A; Molecule type: DNA
A; Residues: 1-193 <LIV>
                                                                                                                    A; Reference number: A; Accession: S70286
                                                                                                                                                                                                                   outer surface protein C - Lyme disease C;Species: Borrelia burgdorferi (Lyme C;Date: 12-Feb-1998 #sequence_revision C;Accession: S70286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-207 </AD>
A;Ressidues: 1-207 </AD>
A;Cross-references: EMBL:X83554; NID:g872027; PIDN:CAA58544.1; PID:g872028
A;Cross-references: EMBL:X83554; NID:g872027; PIDN:CAA58544.1; PID:g872028
A;Cxperimental source: strain PTrob
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Ja:C;Genetics:
                                      A;Cross-references: EMBL:L42897; NID:g858728; PIDN:AAB37006.1; PID:g1695222
                                                                                                 A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: Lyme disease spirochete surface protein F;1-18/Domain: signal sequence \#status predicted <SIG> F;19-207/Product: outer surface protein C \#status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Jauris-Heipke, S.; Liegl, G.; Preac-Mursic, V.; Roessler, D.; J. Clin. Microbiol. 33, 1860-1866, 1995
A; Title: Molecular analysis of genes encoding outer surface prot A; Reference number: I40047; MUID:95395018
A; Accession: S69919
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Borrelia garinii
A;Variety: strain PTrob
C;Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: ospC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: S69919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELTNPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein C - Lyme disease spirochete
rrelia burgdorferi (Lyme disease spirochete)
b_1998 #sequence_revision 20-reb-1998 #text_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                     strain
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1860-1866,
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Pred.
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RESULT 12

RESULT 12

S37727

Outer surface protein C precursor - Lyme disease spirochete
C;Species: Borrelia burgdorfer1 (Lyme disease spirochete)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000
C;Accession: S37727
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschwed. Microbiol. Immunol. 182, 37-50, 1993
A;Title: Genetic heterogenity of the genes coding for the outer surface protein A;Reference number: S37726; MUID:93288136
A;Accession: S37727
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <JAU>
A;Residues: 1-207 <JAU>
A;Cross-references: EMBL:X69595; NID:g311393; PIDN:CAA49305.1; PID:g311394
C;Superfamily: Lyme disease spirochete surface protein C
              RESULT 13
570276
outer surface protein C - Lyme disease spirochete
c:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
C:Accession: S70276
R:Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
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C; Superfamily:
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Best Local Similarity
Matches 140; Conserv
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                                                                                                                                                                                                                                                                                                             GKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFST 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.2%; Score 654; DB 2; llarity 74.5%; Pred. No. 9.4e-24; Conservative 19; Mismatches 25
for lateral transfer and recombination
                                                                                                                                                                        200
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74.58;
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 653; DB 2;
; Pred. No. 1.1e-23
21; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length
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                                                              26-May-2000
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A; Reference number: S70255; MUID:96296448
A; Accession: S70276
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-193 <LIV>
A; Cross-references: EMBL:L42890; NID:9858718
A; Experimental source: Strain E61
C; Genetics:
A; Cross-references: EMBL:A2890; NID:9858718
                                                                                                                                                                                                                                                                                                                                                                                              R:Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994
A:Title: Expression and sequence of outer surface A:Reference number: I40143; MUID:95134673
A:Accession: I40143
                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer surface protein C precursor - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C;Accession: I40143
R;Stevenson, B.; Barthold, S.W.
                                                                                                                                                                                                                                                                            A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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Outer surface protein C precursor - Borrelia garinii
C:Species: Borrelia garinii
C:Species: Borrelia garinii
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 26-May-2000
C:Accession: I40271
R:Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu la
A:Reference number: I40269; MUID:96025162
A;Accession: I40271
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-207 <RES>
A;Cross-references: GB:D49377; NID:g1041103; PIDN:BAA08375.1; PID:g1041104
C:Superfamily: Lyme disease spirochete surface protein C
Search completed: March 18, Job time: 371 sec
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q00137 borrelia he
Q001378 borrelia he
Q002448 borrelia he
Q10411 schizosacch
Q00799 plasmodium
P25386 saccharomyc
P19401 streptcococc
P05659 acanthamoeb
P32399 bacillus su
P12845 caenorhabdi
P13535 homo sapien
P02566 caenorhabdi
Q16787 homo sapien
P02566 caenorhabdi
Q16787 homo sapien
P02567 homo sapien
P02568 plasmodium
Q9aixy rickettsia bu
Q28641 cryctolagus
P17739 borrelia bu
Q28641 cryctolagus
P30622 homo sapien
P02565 gallus gall
P1739 borrelia bu
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P18464 homo sapien
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Q9y623 homo sapien				P34562 caenorhabdi	Q9zlt1 helicobacte		Q99323 drosophila		P29616 gallus gall		P79293 sus scrofa	

ALIGNMENTS

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SEQUENCE FROM N.A. STRAIN-ATCC 35210 / B31; MEDLINE-98065943; PubMed-9403685; MEDLINE-98065943; PubMed-9403685; Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Fraser C.M., Casjens S., Huang W.M., Dodson R., Hickey E.K., Gwinn M., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb JF., Fleischmann R.D., Richardson D., Dougherty B., Tomb JF., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,	SEQUENCE FROM N.A. STRAIN-ANCC 35210 / B31; MEDLINE-96025162; PubMed-7494039; Fikunaga M., Hamase A.; "Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu lato isolates from Japan."; J. Clin. Microbiol. 33:2415-2420(1995).	SEQUENCE FROM N.A. STRAIN-APCC 35210 / B31; MEDLINE-94041630; PubMed-8225587; MEDLINE-94041630; PubMed-8225587; Padula S.J., Sampieri A., Dias F., Szczepanski A., Ryan R.W.; "Molecular characterization and expression of p23 (OspC) from a North American strain of Borrelia burgdorferi."; Infect. Immun. 61:5097-5105(1993).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-ATCC 35210 / B31; MEDLINE-93239332; PubMed-8478108; Wilske B., Preace-Mursic V., Jauris S., Pradel I., Soutschek E., Wilske B., Wanner G.; Schwab E., Wanner G.; "Immunological and molecular polymorphisms of OspC, an immunodominant major outer surface protein of Borrelia burgdorferi."; Infect. Immun. 61:2182-2191(1993).	SEQUENCE FROM N.A. STRAIN-ATCC 35210 / B31; STRAIN-ATCC 35210 / B31; STRAIN-P3268136; PubMed-8098841; MIDLING-93268136; PubMed-8098841; Jauris-Heipke S., Fuchs R., Motz M., Preac-Mursic V., Schwab E., Will G., Wilske B.; "Genetic heterogenity of the genes coding for the outer surface protein C (OspC) and the flagellin of Borrelia burgdorferi."; Med. Microbiol. Immunol. 182:37-50(1993).	_BORBU _BORBU STANDARD; PRT; 210 AA. OSC1_BORBU STANDARD; PRT; 210 AA. Q07337; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) COPTER SURFACE PROTEIN C PRECURSOR (PC). OSPC OR BBB19. Borrelia burgdorferi (Lyme disease spirochete). Plasmid 1p54. Bacteria; Spirochaetales; Spirochaetaceae; Borrelia. NCBI_TaxID-139;

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Smith H.O., Venter
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;; PS00013; PROKAR_LIPOPROTEIN; 1.
embrane; Lipoprotein; Signal; Plasmid;
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OUTER SURFACE PROTEIN C.
N-ACYL DIGLYCERIDE (BY SIMILARITY).
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                                                                                  VARIABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theisen M., Frederiksen B., Lebech A.M., Vuust J., Hansen "Polymorphism in ospC gene of Borrelia burgdorferi and immunoreactivity of OspC protein: implications for taxono use of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
-i- FUNCTION: NOT KNOWN, MAJOR IMMUNODOMINANT PROTEIN.
-i- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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BY SIMILARITY
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N-ACYL DIGLYCERIDE (BY SI)
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                                                                                                                                                                                                                                                                                                                                                                                                    BORHE
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SEQUENCE
SEQUENCE FROM N.A.

STRAIN-SSP. HS1 SEROTYPE 3;

MEDLINE-93133110; PubMed-1484486;

Restrepo B.I., Kitten T., Carter (
"Subtelomeric expression regions")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      Q02448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001800; Lipoprotein_6.

Pfam: PF01441; Lipoprotein_6; 1.

ProDom: PD001149; Lipoprotein_6; 1.

PROSITE; PS00013; PROKAR_LIPOPROTEIN: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SSP. HS1 SEROTYPE 24;
MEDLINE-93133110; PubMed-1484486;
                                                                                                                                                                      Bacteria;
                                                                                                                                                                                            Plasmid
                                                                                                                                                                                                               Borrelia hermsii.
                                                                                                                                                                                                                                         VMP3.
                                                                                                                                                                                                                                                             VARIABLE MAJOR
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FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPI
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el. 26, Last sequence update)
el. 28, Last annotation update)
OUTER MEMBRANE LIPOPROTEIN 3 PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Pred.
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N-ACYL DIGLYCERIDE
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       of Bor
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No. 2.
       Borrelia
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       Infante D., Ba
rrelia hermsii
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.4e-11;
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01-OCT-1996;
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01-OCT-1996;
                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomy
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ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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MO1. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                    Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                     STRAIN-972;
                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                               FROM N.A.
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215 AA;
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(Rel. 34, Last sequence update)
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L 222.8 KDA PROTEIN C1F3.06C IN CHROMOSOME
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Pred. No. 1.7e-10;
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VARIABLE MAJOR OUTER MEMBRANE
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                                                                                                                                              Rajandream M.A., Walsh
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Best Local
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                         "A reticulocyte-binding protein merozoites.";
                                                                                                                                                                                             Plasmodium vivax (strain Eukaryota; Alveolata; Api NCBI_TaxID=31273;
                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seq
01-OCT-1996 (Rel. 34, Last ann
RETICULOCYTE BINDING PROTEIN 2
                                                                                                  Cell 69:1213-1226(1992).
                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=92315338; PubMed=1617731;
                                                                                                                                                                                                                                                                                                                                       PLAVB
                                                                                                                                                                                                                                                                                                            200799;
                                                                                                                                                                                                                                                                                                                       RBP2_PLAVB
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SEQUENCE 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
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                                                    FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECHUMAN RETICULOCYTE CELLS.
SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                       --SSELTKSSEDVKRLTANVETLTQDSKAMKQSFTSLVNSYQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDTSSKLQQL-QLERANFEQKESTLSDENNDLRTKLLKLEESNKSLIKKQEDVDSL-EKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEVETILTSIDELAKAIGKKIKNDVSLDNE-----ADHNGSLISGAYLISNLITKK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQEKLAKSVMQL-----KENEQNFSSLDTSFK--KLNESHQELENNHQTITKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKEMLANSVKELTSPVVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN-AVVLAV
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                                                                                                                                                                                                                                                                                                                       STANDARD;
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, Last annotation updat
PROTEIN 2 (FRAGMENT).
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                                                                                                                                       Ingravallo
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Pred. No. 0.
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                                                                                                                                                                                                         Haemosporida;
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                                                                                  ADHESION. SPECIFICALLY BINDS
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                                                                                                                          Barnwell J. Plasmodium
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RESULT 7
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Best Local S
Matches 104
                            protein
J. Cell
                                                                                                                                                                                                                                                                         USO1_YEAST
P25386;
                                                                                          STRAIN=x2180-1A;
MEDLINE=91185402; PubMed=2010462;
 SEQUENCE OF
                                                                                Nakajima
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                               Eukaryota; Fungi; i
Saccharomycetales;
                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.
                                                                                                                                                                                                                                                                                                                                                           1061
                                                  "A cytoskeleton-related gene, usol,
                                                                   Yamasaki M.;
                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                             1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      JSO1 OR INT1 OR YDL058W
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SGAYL-----ISNLIT--KKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KDNHAQLGIQGVTDENAKKAIL--------KANAAGKDKGVEELEKLSG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DIDSLNTALDELLKKGRTCEVSRYKLIKDTVTKEISDDTELINTIEKNVK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKVALEILAHSDEIDTKQKDSSKLIEMGNQIYLKVVLINQYKNKISSIKSKEEAVSVKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSGKDGNTS--ANSADESVKGPNLTEISKKITDSNAVLLAV-----KEVEALLSSIDEL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVSKKHSELSKITCSDKSYDNITALEKQTELQNLRNSFTQEKTNTNSDSK----LEKIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKYVGIKITPELALTELLGDAKLKTAQELKFESKNNVVLETENMSKNTNELDVHKNIQDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKAIGKKI----
                       transport in Saccharomyc Biol. 113:245-260(1991).
                                                                               H., Hirata A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1251 12
1251 AA;
782-1790 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                        -LKGVIIEVNENTEMNTIESSAKEIEALYNELKNKKTSLNEIYQTSNEVK
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                              Ascomycota; Saccharo; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1251
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                                       Saccharomyces
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                                                                               Ogawa Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 180.5; I
Pred. No. 0.3;
63; Mismatches
                                                                                                                                                                          Saccharomycotina;
                                                                                                                                                                                                                                                                                       PRT;
                                                                            Yonehara
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                                        cerevisiae
                                                                                                                                                                                                                                                                                     1790
                                                    is required
                                                                                                                                                            Saccharomyces
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                                                                               Yoda
                                                    for
                                                                                                                                                                          Saccharomycetes;
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 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hostetter M.K., Herman D.J., Kendrick K.E.; Submitted (FEB-1993) to the E [3]
                                                                    1197
                                                                                                                                        1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X54378; CAA38253.1; -.
EMBL; L03188; AAB00143.1; -.
EMBL; U53668; AAB66659.1; -.
PIR; A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>:</del>
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Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interPro;
                                  251
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COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.
SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEMBRANES. PROBABLY PRESENT ON VESICIER AND THE GOLGI COMPLEX.

DOWAIN: THE RODLIKE TAIL SEQUENCE IS
OF AN HEPTAPEPTIDE BEDDAM CAMMINISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: REQUIRED FOR
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                                                                                                                                                                                                                                                                                                              KEVEALLSSIDELAKAIGKKI-KNDGSLDNEANRNESLLAGAYTISTLITQKLSKLN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; P80220; 1DIP.
S0002216; USO1
TVKIKELQDECNFKEKEVSE-----LEDKLKASEDKNSKYLELQKESEKIKEELDAKT
                                                                KKKNDELEGEVKAMKSTSEEQSNLKKSEIDALNLQIKELKKKNETNEASLLESIKSVESE
                                                                                                                                     NSLRANLESLEKEHEDLAAQLKKYEEQIANKERQYNEEISQLN----DEITSTQQENESI 1196
                                                                                                                                                                     EKLSGSLESLSK-----AA-----KEMLANSVKELTSPVVHGNNSGKDGNTSANSADESV
                                                                                                                                                                                                                                                                           KNIEQLKKTISDLEQTKEEIISKSDSSKDEYESQISLLKEKLETATTANDENVNKISELT
                                IKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSG----ELKAEIEKAKKCSEEFT
                                                                                                                                                                                                       KTREELEAELAAYKNLKNELETKLETSEKALKEVKENEEHLKEEKIQLEKEATET-KQQL
                                                                                                                                                                                                                                           -GSEGLKEKIAAAKKCSEEFSTKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEEL
                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                 ---LTEISKKITESNAVVLAVKEV----ETLLTSIDELAKAIGKK
                                                                                                                                                                                                                                                                                                                                                                9.9%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spectrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    206424
                                                                                                                                                                                                                                                                                                                                                                                                                      COULED COIL (POTENTIAL).

COLILED COIL (POTENTIAL).

CHARGED (HYPER-HYDROPHILIC).

DISPENSABLE FOR THE PROTEIN FU

ASP/GLU-RICH (ACIDIC).

G -> E (IN REF. 2).

E -> K (IN REF. 2).

V -> I (IN REF. 2).

I -> V (IN REF. 2).

N -> S (IN REF. 2).

O -> S (IN REF. 2).

I -> V (IN REF. 2).

R -> S (IN REF. 2).

R -> S (IN REF. 2).

R -> S (IN REF. 2).

C -> S (IN REF. 2).

D -> DEEDDEE (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e EMBL/GenBank/DDBJ
PROTEIN TRANSPORT
                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                              Score 178.5; |
Pred. No. 0.54
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bendel C.M., McClellan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Golgi stack; Cytoskeleton; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ON VESICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSOCIATED WITH INTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIGHLY
                                                                                                                                                                                                                                                                                                                                                                  .54;
                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                156;
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FROM THE E
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                                                                                                                                                                                                                                                                                                                                                63;
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8

Matches 100;

Conservative

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Mismatches

Indels 128;

Gaps

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 Query Match
Best Local Similarity
                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CS24 / Serotype M12;
MEDIANE-88058777; pubMed-2445730;
Robbins J.C., Spanier J.G., Jones
"Streptococcus pyogenes type 12 M
                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
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20-AUG-2001
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                                                                                                                                               DOMAIN
                                                                                                                                                           CHAIN
                                                                                                                                                                         SIGNAL
                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                  Virulence; Phagocytosis;
                                                                                                                                                                                                               PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                   InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
                                                                                                                                                                                                                                                                              PIR; A60115; A60115.
                                                                                                                                                                                                                                                                                         EMBL; M18269; AAA88573.1;
                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L2_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol, 169:5633-5640(1987).

- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SERVED OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: TO OTHER M PROTEINS.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PRO IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHAGOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELKIQLEKITNLSKAKEKSESELSRLKKTSSEERKNAEEQLEKLKNEIQIKNQAFEKER 1369
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                                                                                                                                                                                                                                       PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                            PF02370; M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEROTYPE
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                                                     564
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(Rel. 16, Last sequence up)
(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169:5633-5640(1987)
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                                                                                                                                                                                    Coiled coil;
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62904
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9.6%;
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                                                                                                                                                                                                  Cell wall;
                                                      ¥.
                                                                                                                                                                                 Signal.
 Score 173;
Pred. No. 0
                                                                                        MEMBRANE ANCHOR.
COILED COIL (POTENTIAL).
GLY/PRO-RICH (CELL WALL-SPANNING)
CONSERVED IN GRAM-POSITIVE COCCI
                                                                                                                                              M PROTEIN, SEROTYPE 12.
EXTRACELLULAR (POTENTIAL).
                                                                               PROTEINS
                                                   5F1549DACAA77B46 CRC64;
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                                                                                                                                                                                                  Duplication; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564
                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
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             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     STAPHYLOCOCCAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulation
            Length 564;
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ation by
                                                                                           COCCI SURFACE
                                                                                                                                                                                                  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         upstream
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                                                                                                                                                                                                                                                                                                                                                                                    outstation
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MYSN_ACACA
ID MYSN_A
AC P05659
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                                                                                                                                                                                                                                                                                                                                                                       Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;
"Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle myosin heavy chain gene from Acanthamoeba: evidence of a hinge in the rodlike tail.";

J. Cell Biol. 105:913-925(1987).

-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

-I- SUBDNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
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       modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1988 (Rel. 09, Las
20-AUG-2001 (Rel. 40, Las
MYOSIN II HEAVY CHAIN, NO
Acanthamoeba castellanii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87308395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988 (Rel. 01-NOV-1988 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P05659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
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                                                                                                                                           SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR SIMILARITY: CONTAINS 2 IQ DOMAINS.
                                                                                                                                                            CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILDIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.
MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                   DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE,
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PROSITE: PS50096; IQ; 1.

Myosin; Coiled coil; Actin-binding; ATP-binding; Calmodulin-binding; Myosin; Coiled coil; Actin-binding; Multigene family.

Methylation; Alkylation; Phosphorylation; Multigene family.

MYOSIN HEAD-LIKE.
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Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOm; PD000355; myosin_head; 1.
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Bacillus/Staphylococcus
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Submitted (JUN-1997)
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M97208; AAA22521.1;
Z99109; CAB12856.1;
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n; Transmembrane;
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PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB).
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ne EMBL/GenBank/DDBJ (
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Pred. No. 0.
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434
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RESULT 11
MYSC_CAEEL
C -!- FUNCTION: MUSCLE CONTRACTION.

C -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

C HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

C HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2),

C HEAVY CHAIN SUBUNITS (MIC-2),

C -!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

C -!- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

C -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE HEAVXNOEAL MUSCLE.

C -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE MYOFIBRILS, SHWING

C (YCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C C CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

C -!- PIM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

SELIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYSC_CA
P12845;
                                                                                                                                                           modified and this statement entities requires a license
                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karn J., Dibb N.J., Miller D.M.; "Cloning nematode myosin genes."; Cell Muscle Motil. 6:185-237(1985).
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20-AUG-2001
                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BRISTOL N2;
MEDLINE=85201409; PubMed=3888374;
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                                                                                                  EMBL;
                                                                                                                EMBL;
                                                                                                                                                 or send an
                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN
                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS:
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                                                            L; M37233; AAA28121.1; -.
L; M37233; AAA28122.1; -.
L; M37235; AAA28122.1; -.
                                                                                                                                                                                                                                                                                                    ELEGANS
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                                             ; M37233; AAA28121.1;
; M37235; AAA28122.1;
; M37236; AAA28123.1;
S05697; S05697.
                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboratien the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                               equires a license agreement (See email to license@isb-sib.ch).
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PubMed=2926820;
ama I.N., Krause M., Karn J.;
יייה המmplete Caenorhabditis elegans myosin
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EMBL; PIR;

InterPro;

IPR002928; IPR001609;

Myosin_tail.
myosin_head.

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HSSP; P08799;

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MYH8_HUMAN
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Best Local S
Matches 93
TISSUE-Skeletal muscle;

MEDLINE-90323631; PubMed=2373371;

Karsch-Mizrachi I., Feghali R., S

"Generation of a full-length huma"
                                                                                                                      P13535; Q14910;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, SKELETAL MUSCLE, PERINATAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
MOD_RES
MOD_RES
CONFLICT
CONFLICT
SEQUENCE
                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                         Homo
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P13535; Q1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00193; MYOSINHEAVY ProDom; PD000355; myosin_hea
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PF01576;
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                                               FROM N.A.
                                                                                                                                                                                                                                                                                      -LEKKQKAFDKVIDEWKKKVDDLYLELDGAQRDARQLSGEAHKLRGQHDTL----
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                                                                                                                                                                                     STANDARD;
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Myosin_tail;
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> D (IN REF. 2).
M -> I (IN REF. 2).
  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E -> D (IN REF. 2).
M -> I (IN REF. 2).
MW; 6D65AE99BD013627
                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 169.5;
Pred. No. 1.5
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ATP (BY SIMILARITY).
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           Shows T.B.
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                                                                                 Hominidae;
             Jr.,
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  myosin
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             Leinwand L.
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Pfam; Pfam; Pfam;

PF01576;

myosin_head;
Myosin_tail; IQ; 1

MYOSINHEAVY

PD000355; PR00193; InterPro;

; IPR000048; ; IPR002928; ; IPR001609;

Myosin_tail.
myosin_head.

PF00612;

EMBL;

AF067143; AAC21557.1;

PIR; A30220; A30220 HSSP; P13538; 2MYS.

MIM; 160741;

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RA ESSET K., Tidhar A., Myszkowski M.;

RY TISOLation and characterization of the human perinatal MHC promoter.";

RI Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

CC :- FUNCTION: MUSCLE CONTRACTION.

CC :- SUBUNIT: MUSCLE CONTRACTION.

CC :- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS OF THE MYOFIBRILS.

CC :- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

CC :- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

CC :- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

CC :- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.

CC C CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC C CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC C CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC C PYM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC ALKYLATED AND ARE REGUIRED FOR MYOSIN ATPASE ACTIVITY LIGHT

CC ALKYLATED AND ARE REGUIRED FOR MYOSIN ATPASE ACTIVITY.

CC ALISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC THISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC THISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

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                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSER K., Tidhar A., Myszkowski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feghali R., Leinwand L.A.;
"Molecular genetic characterization o
human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
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MEDLINE=95324556; PubMed=7601129;
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Gene 89:289-294(1990).
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, M36769; AAC17185.1;
, Z38133; CAA86293.1;
, X51592; CAA35941.1;
, M35250; AAA36346.1;
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                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                the
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SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
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                                       Caenorhabditis elegans
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A -> R (IN REF. 2)
E -> Q (IN REF. 1)
M -> N (IN REF. 1)
M -> N (IN REF. 3)
N -> H (IN REF. 3)
N -> DGG (IN REF. 1)
MC -> DGG (IN REF. 1)
MC -> Q (IN REF. 1)
K -> Q (IN REF. 1)
K -> AH (IN REF. 3)
EN -> AH (IN REF. 2)
D -> H (IN REF. 2)
WH: ABEE2D151792E9
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Pred. No. 1
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   Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> D (IN REF. 1 AND 4).
-> H (IN REF. 2).
; A3EE2D151792E9E8 CRC64;
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(SH-2) (
REF. 2).
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AND 4).
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McLachlan A.D., Karn J.;
"Periodic charge distributions in the
"Periodic charge distributions in muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                         Myosin; Muscle procesu; control ATP-binding; Methylation;
                                                                                                                                                                                                                                             PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                   InterPro; IPR002928; Myosin
InterPro; IPR001609; myosin
Pfam; PF00063; myosin_head;
Pfam; PF01576; Myosin_tail;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J01050; AAA28124.1;
EMBL; V01494; CAA24738.1;
PIR; A02992; MWKW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement
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[1]
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                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P08799; 1MND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
DOMAIN: THE ROLLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASES ACTIVITY.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN (CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: MUSCLE CONTRACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFRAGMENT (S2).
851
1165
1165
177
665
769
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PubMed=7202124;
850
1966
1164
1176
1966
1966
184
687
                                                                                                                                                                                                                                                                                                                                                                        myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                  Myosin_tail
                                                                                                                                                                                                                           Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                   Alkylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Karn J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is not removed.
                                                                                                                     MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
LIGHT MEROMYOSIN (LMM).
ATP (BY SIMILARITY).
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                   HINGE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions ong as its content is in over the content is in over the content in the content is the content in th
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Best Local S
Matches 97
                                                                                                                                                                                  LMAA HUMAN STANL....

LMA3_HUMAN STANL....
Q16787; Q13679; Q13680;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                 TISSUE-Keratinocytes; MEDLINE-94357926; PubMed-8077230; Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.; "Cloning of the Lamma gene encoding the alpha 3 chain ligand epiligrin. Expression in wound repair."; J. Biol. Chem. 269:22779-22787(1994).
            "Cloning
                       Uitto J.,
                               Vidal F., Baudoin
                                        SEQUENCE OF 1-1331 FROM N.A. (ISOFORMS MEDLINE=96163880; PubMed=8586427;
                                                                                                                                                                                                                                                                                                                 1521
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MOD_RES
MOD_RES
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CONFLICT
SEQUENCE
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1181
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                                                                                                                                                                                                                                                                                                                                     VKELT
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                                                                                                                                                                                                                                                                                                                                                       IDEWRKKTDDLAAE----LDGAQRDLRNTSTDLFKAKNAQEELAEVVEGLRRENKS-LSQE 1520
                                                                                                                                                                                                                                                                                                                                                                                              AQKINELQEALDAANSKNASLEKTKSRLVGDLDDAQVDVERANGVASA-LEKKQKGFDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                         QHEAEQLQESLEEEIEGKN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIAA-----AKKCSEEFSTKLKDNHAQLG-----IQGVTDENAKKAILKANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDGQSRISELEEELENERQSRSKADRAKSDLQRELEELGEKLDEQGGATAAQVEVNKKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDGNTSANSADESVKGP-------NLTEISKKITDSNAVLLAVKEVEALLS
  , Baudoin C., Miquel C., Galliano
, Ortonne J.-P., Meneguzzi G.;
of the laminin alpha 3 chain gene
ozygous deletion in a patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             NDV--SLDNEADHNGSL-ISGAYLISNLITKKISAIKDSGELKAEIEKAKKCSEEF
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1880
1966
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715
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Pred.
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
MW; B66F0BB2FE27B67F CRC64;
                                                                                                                                                                   Catarrhini;
                                                                                                                                                                             Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ± 167;
  gene
with
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                               M. -F.,
  (LAMA3)
Herlitz
                                                                                                                                                                   Hominidae;
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                                                   В
                                                                                           3 chain
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          identification
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В ρ Вb δÃ В QV B Š

SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTIN DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WITO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END THE ALPHA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILIGRIN/KALININ/NICERN), AND POSSIBLY ALSO A COMPONENT OF LAMININ-6 (K-LAMININ) AND LAMININ-7 (KS-LAMININ). CONSISTING OF THREE GAMMA), WHICH ARE BOSS-SHAPED MOLECULE

: THE BASEMENT

-SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN MEMBRANES (MAJOR COMPONENT).
ALTERNATIVE PRODUCTS: THE TWO ISOFORMS A AND E THE RODUCTS: THE TWO ISOFORMS A AND B DI DIFFER SMALLER VARIANT

TISSUE SPECIFICITY: SKIN; RESPIRATORY, URINARY, AND DIGESTIVE EPITHELIA AND IN OTHER SPECIALIZED TISSUES WITH PROMINENT SECRETORY OR PROTECTIVE FUNCTIONS. EPITHELIAL BASEMENT MEMBRANE, AND EPITHELIAL CELL TONGUE THAT MIGRAPES INTO A WOUND BED. A DIFFERENTIAL AND FOCAL EXPRESSION OF THE ALPHA-3 CHAIN IS OBSERVED. OBSERVED

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VQ.

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INDUCTION: LAMININ-5 IS UP-REGULATED IN WOUND SITES OF HUMAN SKIN. DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

DOMAIN: DOMAIN G IS GLOBULAR.

DOMAIN: DEFECTS IN LAMA3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS

SIMILARITY: SIMILARITY: CONTAINS 2.5 LAMININ EGF-LIKE DOMAINS.
5 LAMININ G-LIKE DOMAINS.

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Pfam: PF00054; laminin_G; 2.
SMART; SM00180: EGF_Lam; 2.
SMART; SM00282; LamG; 5.
SMART; SM00210; TSPN; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1. InterPro; IPR000561; I InterPro; IPR002049; I InterPro; IPR001791; I InterPro; IPR003129; T Glycoprotein; Basement membrane; Extracellular matrix; Laminin EGF-like domain; Cell adhesion; Repeat; Signal Alternative splicing; Epidermolysis bullosa. Alternative SIGNAL Pfam; EMBL; EMBL; MIM; 226700; ; L34155; AAA59483.1; X85107; CAA59428.1; X85108; CAA59429.1; P02468; TTLE. PF00053; splicing; laminin_G; 2. laminin_EGF; 2.
laminin_G; 2. TSPN Laminin_G. Laminin_EGF. EGF-like Coiled

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DOMAIN
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                                                                                                                            DNHAQLGIQGYTDENAKKAIIKANAAGKDKGYEELEKLSGSLESLSKAAKEMLAN-SYKE : :|| | || : ||: ||: || :| : || |
                                                                                                                                                                                                                                                                                                            ENNGLANSIRDS-----LNEYEAKLSDLRARLQEAAAQAKQANGLNQENERALGAIQRQV
                                                                                                                                                                                                                                                                                                                                                         DGNTSANSADESVKGPNLTEISKKITDSNAVL----LAVKEVEALLSSIDELAKAIGKKI
LVRCAVDAATAYENILNAIKAAEDAANRAASASES
                                             LT-----SPVVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKE
                                                                                                                                                                                                          KEINSLQSDFTKYLTTADSSLLQTNIALQLMEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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23.0%;
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W -> R (IN REF. 2).
ATG -> GMC (IN REF. 2).
M -> K (IN REF. 2).
R -> L (IN REF. 2).
E -> Q (IN REF. 2).
D -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                  Score 166.5; L
Pred. No. 1.7;
71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                71;
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LAMININ G-LIKE 2.

LAMININ G-LIKE 3.

LAMININ G-LIKE 4.

LAMININ G-LIKE 4.

LAMININ G-LIKE 5.

COILED COIL (POTENTIAL).

BY SIMILARITY.

BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5 X LAMININ EGF-LIKE REPEATS.
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3 (INCOMPLETE).
DOMAIN II AND I (HEPTAT REPEATS).
5 X LAMININ G-LIKE REPEATS (DOMAIN G).
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FOR STATEMENT 
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2.5 X LAMININ EGF-LIKI
                                                                                                                                                                                                        SQKEYEKLAASLNEARQELSDKVR
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) (POTENTIAL).
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(POTENTIAL).)
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RESULT 15
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01-APR-1993
01-OCT-1996
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SEQUENCE FROM N.A.
MEDLINE-92315338; PubMed-1617731;
Galinski M.R., Medina C.C., Ingravallo P
Galinski M.R., Medina protein complex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID=31273;
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Q00798;
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SUBUNIT: HOMODIMER (POTENTIAL).
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Pred. No. 3.4;
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Search completed: March 18, 2002, 10:11:52 Job time: 970 sec

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SP_archea:*

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sp_human:

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sp_manm;

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Local Similarity 98.9%;
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ALIGNMENTS

O31114 PRELIMINARY; O31114; 01-JAN-1998 (TrEMBLrel. 0 01-JAN-1998 (TrEMBLrel. 0 01-JUN-2001 (TrEMBLrel. 1 OUTER SURFACE PROTEIN C (wang I.N., Dykhuizen D.E., Dunn J.J., Luft B.J.; submitted (CCT-1997) to the EMBL/GenBank/DDBJ data EMBL; AF029861; AAB86544.1; InterPro.; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD01441; Lipoprotein_6; 1. NON_TER 194 194 Borrelia burgdorferi (Lyme disease spirochete). Bacteria; Spirochaetales; Spirochaetaceae; Borr NCBI_TaxID=139; SEQUENCE FROM N.A. STRAIN=OC2; 194 194 AA; 194 20452 MW; 05, Created) 05, Last sequence update) 17, Last annotation update) (FRAGMENT). PRT; 712A6C5B7873C21F CRC64; 194 ጅ Borrelia databases

2

Score 903; DB 2; Pred. No. 2.8e-33; 2; Mismatches 0

0;

0;

Gaps

0

66

126 120

186

Length 194 Indels

Db dq

181 187

KELTSPVV

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STRAIN=OC10;
Wang I.-N., Dykhuizen D.E.,
Submitted (OCT-1997) to the
EMBL; AF029869; AAB86552.1;
                                                                                                                                                             Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
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                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=139;
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Jauris-Heipke S., Liegl G., Preac-Mursic V., Roessler D., Schwab E Soutschek E., Will G., Wilske B.;

"Molecular analysis of genes encoding outer surface protein C (osp evidence of lateral gene exchange of ospC.";

J. Clin. Microbiol. 33:1860-1866(1995).

InterPro; IPR01800; Lipoprotein_6.

Pfam; PP01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

Prodom; PD001149; Lipoprotein_6; 1.
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01-NOV-1996 (TremBLrel. 01,
01-JUN-2001 (TremBLrel. 17,
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ales; Spirochaetaceae; Borrelia
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Spirochaetaceae; Borr
             Dunn J.J., Luft B.J.; EMBL/GenBank/DDBJ databases.
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Mol. Microbiol. 18:257-269(1995).
EMBL; L42868; AAB37011.1;
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
                                                                                                                                                                                                                                                                                                                                                    P94242; PRELIMINARY; PRT; 193 AA. P94242; 01-MAY-1997 (TrEMBLrel. 03, Created) 01-MAY-1997 (TrEMBLrel. 03, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation OUTER SURFACE PROTEIN C (FRAGMENT). OSPC.
      121
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Spirochaetaceae; Bor
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Pred. No. 1.9e-32;
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01-NOV-1996
01-JUN-2001
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Q9S3P2;
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Q44719;
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Mol. Microbiol. 18:257-259(1995).
EMBL; L42893, AAB37001.1;
Interpro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0UTER SURFACE PROTEIN C (FRAGMENT).
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
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Bacteria; Spirochaetales; S
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    Stevenson B.,
                   MEDLINE-95154673; PubMed-7851744;
                                                               SEQUENCE FROM N.A.
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nilarity 99.48;
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Matches 180;
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01-JUN-2001 (TI
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EMBL; U04281; AAC43297.1; -.

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 210 AA; 22526 MW; 2D672991D584E4EE CR
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Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

Signal; Lipoprotein; Outer membrane
SIGNAL 1 18 POTENT
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203
203 AA;
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21364
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                                                                                                                                                       47.78;
                                                                                                                                                                                                                                                                                                                                           Outer membrane.

18 POTENTIAL.

OJ OUTER SURFACE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01, Created
01, Last so
17, Last and
17, PRECURSOR
                                                                                                                                                                                                                                                                                    XW.
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                                                                                                                       Score 862; DB Pred. No. 1.9e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
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No. 3.
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etaceae; Borrelia
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.9e-31;
les 5;
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.4e-32;
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Best Local Similarity
                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TREMBLrel. 17, Last annotation updat
0UTER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel
  STRAIN-TETS
                          SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=139;
                                                                                                                                                                                                                                                           Q9R7B3;
                                                                                                                                                                                                                                                                                      Q9R7B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Evolution of the Borrelia burgdorferi
J. Bacteriol. 177:3036-3044(1995).
EMBL; X84765; CAA59236.1; ...
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
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Q44980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Spirochaetales;
NCBI_TaxID=139;
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178 i
                                                                                                                                                                                                                                                                                 PRELIMINARY;
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18724 MW;
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Spirochaetaceae; Bor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 849; DB 2
Pred. No. 6e-31;
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Q9AGB1;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                           Lawson C.L., Swaninathan S.;
"Crystal structure of outer surface protein disease spirochete, Borrella burgdorferi.";
EMBO J. 0.0-0(2001).
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                                                                                                                                                                                                                                                                               STRAIN-HB19;
                                                                                                                                                                                                                                                                                                                                    Bacteria;
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Ras N.M., Postic D., Foretz M., B.
"Borrelia burgdorferi sensu stric
U.S.A.'?";
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MSGAYLISTLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAK
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162; Conserv
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                                                                                                                                                                                    AF337548; AAK21289.1;
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1 (TrEMBLrel. 17,
1 (TrEMBLrel. 17,
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174 AA;
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Spirochaetaceae; Borrelia
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stricto,
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Pred. No. 2.3e-28;
3; Mismatches 2
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56E01536D22F61BF
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O31115;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
OSPC.
STRAIN-OC3; Wang I.-N., Dykhuizen D. Submitted (OCT-1997) to EMBL; AF029862; AAB86545
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Ras N.M., Postic D., Foretz M., B.
"Borrelia burgdorferi sensu stric
U.S.A.'?";
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01-JAN-1998 (TrEMBLrel. 05, Last sequence updat
01-JUN-2001 (TrEMBLrel. 17, Last annotation upd
0UTER SURFACE PROTEIN C (FRAGMENT).
BOTTella burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
NCBI_TaxID-139;
                                                                                                                           Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; SCBI_TaxID=139;
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he EMBL/GenBank/DDBJ
                                                                                                                                                   s disease spirochete).
Spirochaetaceae; Born
  Dunn J.J., Luft B
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stricto, a bacterial
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Pred. No. 5e-28;
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Submitted (OCT-1997) to the EMBL/Ger
EMBL; AF029871; AAB86554.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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                           TKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANS
                                                                 IGKKIKNDGSLDNEANRNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFS
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                   KKLEGEHAQI
                                                        IGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFT
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194 AA;
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193 1
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75.1%;
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Spirochaetaceae;
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Pred. No. 9.1e
19; Mismatches
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EMBL/GenBank/DDBJ
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Pred. No. 2.9e-25;
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9.1e-23;
hes 26;
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databases.
                                                                                                                                                    Length 194;
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186

VKELTSPIV

194

034120

PRELIMINARY;

184 A

Last sequence update)

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RESULT 15
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ID P94234
AC P94234
AC P94234
DT 01-MAY
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DE OUTER
GN OSPC.
OS BORTCEL
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Best Local Similarity
Matches 142; Conserv
SEQUENCE FROM N.A.
STRAIN-28354;
MEDLINE-96296448; PubMed-8709845;
                                                                            Borrelia burgdorferi (Lyme Bacteria; Spirochaetales;
                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
01-TER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marti-Ras N., Postic D., Foretz M., Baranton G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U91793; AAB81890.1;
Interpro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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01-JAN-1998 (TYEMBLEL 05, Last sequence updatol-1-JUN-2001 (TYEMBLEL 17, Last annotation updouter SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia burgdorferi (Lyme disease spirochete).
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Ras N.M., Postic D., Foretz M., Baranton G.;
"Borrelia burgdorferi sensu stricto, a bacterial species 'made in U.S.A.'?";
                                                               NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=TETS;
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[2]
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llarity 76.3%;
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Spirochaetaceae; Bor
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EMBL; L42895; AAB37003.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                      Livey I., Gibbs C.P., Schuster R., "Evidence for lateral transfer and Lyme disease Borrelia.";
                   182
                                      121
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180
                                                                                                                                                   Local Similarity 75.9%;
hes 142; Conservative
                                                                          LKDNHAQLGIQGYTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLANSVK 181
ELTSPIV
                  ELTSPVV
                                      LEGEHAQLGIENVTDENAKKAILITDAA-KDKGAAELEKLFKAVENLAKAAKEMLANSVK 179
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193 AA;
186
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; Pred. No. 1.1e-22;
17; Mismatches 26
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Search completed: March 18, Job time: 977 sec 2002, 10:10:54

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Title:
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Maximum DB
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Maximum Match 100%
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1476
1225.5
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ALIGNMENTS

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RESULT AAB6717 ID AAB6 XX AAB6 XX AAB6 XX AAB6 XX BOIT O3-A XX BOIT XX BOIT XX BOIT XX BOIT XX BOIT XX WAD1; DR WAP1; DR WAP2 XX WAD1; DR WAP2 XX Comm PT Lymm Chimeric - Borrelia sp. Chimeric - Borrelia sp. WPI; 2001-050113/06. N-PSDB; AAF29021. Dattwyler RJ, 18-JUN-1999; 19-JUN-2000; 2000WO-US16915 Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick Borrelia sp chimeric ospC protein SEQ ID NO: 03-APR-2001 (first entry) AAB62717; AAB62717 standard; Protein; (UYNY) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC. 28-DEC-2000. WO200078966-A1 ب Seinost G, 9905-0140042 Dykhuizen D, 368 ₽ Luft BJ, 38 Gomes-Solecki M;

2001-050113/06

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(BROO-)
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Chimeric -
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                                                                                                           Borrelia
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Lyme disease are used
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Borrelia
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; Pred. No. 1.2e-87;
24; Mismatches 31; I
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Lyme disease are used
to Lyme disease -
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Lyme disease are used
to Lyme disease -
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d to immunize animals and detect immune responses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; tick
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            The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
                                                                        Chimeric -
Chimeric -
                                                          Claim 43; Page 133-134; 160pp; English
                                                                                                      WPI; 2001-050113/06.
N-PSDB; AAF29036.
                                                                                                                                                                  18-JUN-1999;
                                                                                                                                                                                19-JUN-2000;
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                                                                                                                                                                                                                                                   Borrelia; ospC;
                                                                                                                                                                                                                                                                 Borrelia
                                                                                                                                                                                                                                                                                 03-APR-2001
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                                                                                                                             Dattwyler RJ,
                                                                                                                                           (UYNY ) UNIV NEW YORK STATE RES
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                                                                                                                                                                                                                             Borrelia
                                                                                                                                                                                                                                    Borrelia
                                                                                                                                                                                                                                                                 chimeric ospC protein
                                                                                                                                                                                 2000WO-US16915
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                                                                                                                                                                                                                                                   Lyme disease;
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                                                                                                                                                                                                                                                   chimeric protein;
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                                                                                                                              ъJ,
                                                                                                                              Gomes-Solecki M;
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Query Match
Best Local S
Matches 309
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mes 309; Conservative
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                                                  KLKSEHAVLGLDNLTDDNAQRAILKKH-ANKDKGAAELEKLFKAVENLSKAAQDTLKNAV
                                                                                KELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASI
                                       keltspvvhgnnsrkdgnastnsadesvkgpnlteiskkitesnavvlavkevetllasi
                                                                                                                                                                                                                      393 AA;
                                                                                                                                                                   82.1%; Score 1476; DB 22;
83.5%; Pred. No. 5.1e-87;
Live 26; Mismatches 31;
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Matches 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease \cdot
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                           to Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 43;
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Chimeric -
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                                                                                                                                                                                                                               Local Similarity
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                                                                                                                   KLKSEHAVLGLDNLTDDNAQRATLKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK
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DB; AAF29017.
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Borrelia
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                                                                                                                                                                                                       Score 1225.5; DB 22; Length 377;
Pred. No. 4.9e-71;
13; Mismatches 61; Indels 11;
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Matches Query Match Best Local

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68.1%; 70.2%;

Conservative

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Score 1224; DB Pred. No. 6e-71; 2; Mismatches

22; 61;

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                           The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
 Sequence
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                                                                                                     Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                                                    N-PSDB;
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Chimeric -
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                                                                             Claim 43;
                                                                                                                                                                Dattwyler RJ,
                                                                                                                                                                                  (UYNY ) UNIV N
(BROO-) BROOK
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                                                                                                                                                                                                                                                                                                                     Borrelia; ospC; Lyme disease;
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                    disease.
                                                                                                                                     AAF29015
                                                                                                                                                                                             UNIV NEW YORK STATE RES
                                                                          Page 81; 160pp; English
 373 AA;
                                                                                                                                                                                                                                                                                          Borrelia
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                                                                                                                                                                                    BIOTECHNOLOGIES
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                                                                                                                                                                                    INC.
                                                                                                                                                                                                                                                                                                                    vaccine; chimeric protein; tick.
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                      The present invention provides compositions comprising ospC proteins chimeric ospC proteins from members of the Borrelia genus. These may Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and lea
                                                                 Claim 43;
                                                                                 Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                                                                                                                                                                      18-JUN-1999;
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                                                                                                                    N-PSDB;
                                                                                                                                           Dattwyler RJ,
                                                                                                                                                           (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                               Borrelia; ospC; Lyme disease; vaccine;
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DB; AAF29033.
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                                                                Page 125-126;
                                                                                                                                                                                                                                                       Borrelia
Borrelia
                                                                                                                                                                                                                                                                                                chimeric
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                            Seinost
                                                                                                                                                                                     9905-0140042
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                                                                                                                                                                                                                                                                                                                                                   Protein; 397
                                                                                                                                                                                                                                                       sp.
                                                                                                                                                                                                                                                                                               ospC protein SEQ
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                                                               160pp;
                                                                                                                                           Dykhuizen
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                                                                                                                                                                                                                                                                                                 ID NO:
                                                                                                                                                                                                                                                                              chimeric protein;
                                                                                                                                          Luft
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                                                                                         of Borrelia which detect immune respo
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                                                                                                                                            Gomes-Solecki
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Query Match

67

.98;

Score

1221;

DB

22;

Length

397;

The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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Sequence

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Lyme

disease.

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RESULT 1
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                                                              Compositions of OspC |
Lyme disease are used
to Lyme disease -
                                                                                                                                                                                                                                                   Chimeric - Chimeric -
                                                                                                                                                                                                                                                                                                                  03-APR-2001
                                              Claim 43;
                                                                                                   N-PSDB; AAF29020
                                                                                                                              Dattwyler RJ,
                                                                                                                                                         (UYNY )
                                                                                                                                                                           18-JUN-1999;
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                                                                                                                                                                                                                                                                               Borrelia;
                                                                                                                                                                                                                                                                                               Borrelia sp chimeric
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                                                                                                            2001-050113/06
                                                                                                                                                 BROOK
                                                                                                                                                         UNIV NEW YORK STATE RES FOUND
                                              Page 94-95;
                                                                                                                                                                                                                                                                              ospC; Lyme
                                                                                                                                                                                                                                                  Borrelia
Borrelia
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                                                                                                                                                 BIOTECHNOLOGIES
                                                                                                                               Seinost
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                                                                       polypeptides from strains of Borrelia which cause is to immunize animals and detect immune responses
                                                                                                                                                                                                                                                                               disease;
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3; Mismatches
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Lyme disease.

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Matches
                                                                                            WPI; 200
N-PSDB;
                            Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                                                                                                                                      (UYNY )
(BROO-)
                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Borrelia sp. Chimeric - Borrelia sp.
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61; Conservative
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70.58;
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Matches 261
WPI; 2001-050113/06
                   Dattwyler RJ,
                                                                                                                                                     Chimeric -
Chimeric -
                                                                                                                                                                              Borrelia; ospC; Lyme disease; vaccine; chimeric protein;
                                     (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                                         19-JUN-2000; 2000WO-US16915
                                                                                                             28-DEC-2000
                                                                                                                                 WO200078966-A1
                                                                                                                                                                                                      Borrelia sp
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                                                                      18-JUN-1999;
                                                                                                                                                                                                                                                AAB62731;
                                                                                                                                                                                                                                                                 AAB62731 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
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Lyme disease are used to
to Lyme disease -
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46; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 43; Page 83-84;
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7; Mismatches 6!
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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   US-08-235-836C-110
US-08-158-353-2
US-08-235-836C-107
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US-08-235-836C-30
US-08-235-836C-30
US-08-235-836C-31
US-08-209-603E-15
US-08-209-603E-15
US-08-209-603E-11
US-08-235-836C-34
US-09-196-293-11
US-08-235-836C-36
US-08-235-836C-36
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US-08-235-836C-36
US-08-235-836C-36
US-08-235-836C-36
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US-08-482-847-23
US-08-482-847-23
US-08-471-491-5
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US-08-477-451-3
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US-08-735-893-4
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Sequence 12, App
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Sequence 32, Appli
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Query Match 37.5 Best Local Similarity 44.9 Matches 173; Conservative

37.5%;

; Score 673; DB 4; I; Pred. No. 1.3e-45; 58; Mismatches 112;

Length 466; Indels 42;

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	36C-110 110, Application US 110, Application US 110, Application US ANT: Dunn, John J. ANT: Dunn, John J. ANT: Luft, Benjami OF INVENTION: NO. OF SEQUENCES: 144 PONDENCE ADDRESS: ESSEE: Brookhaven ET: Upton E: Upton ET: Upton ER READABLE FORM: UTER: IBM PC Compa ATING SYSTEM: PC-D WARE: Patentin Rel T APPLICATION DATA: SIFICATION NUMBER: US NG DATE: 29-APR-19 WARE: PATENTON DATA: SIFICATION NUMBER: US NG DATE: 01-11-93 EY/AGENT INFORMATIO: BOGOSIAN, MATGEN MANUALCATION INFORMATIO: BOGOSIAN, MATGEN STRATION NUMBER: US FAX: (516) 282-7 ION FOR SEQ ID NO. CE CHARACTERISTICS: CE CHARACTERISTICS: CE TYPE: protein 36C-110		777777777777777777777777777777777777777
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	ion US/08235836C ohn J. enjamin	ALIGNMENTS	US-08-973-462-8 US-08-053-614-2 US-09-034-306-2 US-09-034-306-2 US-09-053-614-4 US-08-053-614-4 US-08-053-614-4 US-08-053-614-4 US-08-153-614-4 US-09-259-437-4 PCT-US93-09782-4 US-08-328-254-6 US-08-328-254-6 US-08-328-254-6 US-08-214-164-2 US-08-246-636-2 US-08-246-636-2 US-08-247-491A-3 US-08-247-491A-3 US-08-247-491A-3 US-08-319-795-2
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-158-353-2
Matches
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; Sequence 2, Applicati
; Patent No. 5620862
; GENERAL INFORMATION:
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                                                           Query Match
Best Local Similarity
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
NAME: Garroll, Alice 0.
TOTAL OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                     Score 657.5;
Pred. No. 7.
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                            Mismatches
                        nes 29;
                                                                              DB 1;
                                                                              Length 212;
                  Gaps
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Best Local Similarity
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1:
Patent No.
                                                                                                                                                                                                                                                                             TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-11-93
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APPLICATION NUMBER: US/08/235,836C

FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                         55
                                                                                                                                                                                                                                                                                                                                                           NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324 REFERENCE/DOCKET NUMBER: BN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 VKELTSPIVHGN 189
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                                                         9
                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Upton
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ELATKAIGKKIGNNG---LEANQ-SKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTA 110
                                                                             GKDGNASANSADESVKG-----PNLTEISKKITESNAVVLAVKEVET----LLASID 54
                                                  GSQKENDLNLEDSSKKSHQNAKQDLPAVTEDSVSLFNGNKIFVSKEKNSSGKYDLRATID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLKSEHAVLGLDN--LIDDNAQRAILKKHANKDKGAAELEKLEKAVENLSKAAQDILKNA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEFTN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISCNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDEVAKKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122, Application US/08235836C
). 6248562
                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                 588 amino acids
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Luft, Benjamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brookhaven National Laboratory
                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-APR-1994
V: 435
                                                                                                                                35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 6248562el Chimeric Proteins Comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/148,191
                                                                                                                    55;
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                                                                                                                                                                                                                                                                                                                                                            BNL93-28A
                                                                                                                Score 640; DB 4;
Pred. No. 6.8e-43;
5; Mismatches 110
                                                                                                                  110;
                                                                                                                                               Length 588;
                                                                                                               Indels 122;
                                                                                                               Gaps
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US-08-235-836C-107; Sequence 107; Application US/08235836C; Patent No. 6248562; GENERAL INFORMATION:
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; MOLECULE TYPE: US-08-235-836C-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                              TELEFAX: (516) 282-37: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acid
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$2,08/235,836C
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
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                                                                                                                                                            NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTVEIKEGTVTLKREIEKDGKVKVFLNDTAGSNKKTGKWEDSTSTLTISADSKKTKDLVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTDGTTTVQQYNTAGTSLEGSASETKNLSE-----LKNALK--GHPM--GNNSGKDGNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVELKGTSDK--NNGSGTLEGSKPDKSKVKLTVSADLNTVTLEAFDA-SNQKISSKV-TK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIVHGNNSRKDGNAS
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                                                            466 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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               protein
                                                                                                           282-3729
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Query Match

35.5%;

Score 638.5;

DB 4;

Length 466;

β 2

17

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APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Motz, Manfred
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
TITLE OF INVENTION: Active proteins from Borrella
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 009/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1990-12-22
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
NUMBER: DE SEQ ID NOS: 16
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                                                                                                   ; ORGANISM: Borrelia
US-09-196-293-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09196293 Patent No. 6183755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 44.6%; matches 166; Conservative
                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15
                   Query Match
Best Local Similarity
Matches
                                                                                                                                         LENGTH: 20
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 EVFKEDGKTLVSKKVTSKDKSSTEEKFNEKGEVS-EKIITRADGTRLEYTGIKSDGSGKA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 DTLKNAVKELTS 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 QCSTEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQ 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCSETFTNKLKAKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDELATKAIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDSTSTLTISADSKKTKDLVFLTDGTITVQQYNTAGTSLEGSASEIKNLSE-----LKNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMLANSVKELTS
                                                                                                                                                              209
Conservative
                                                                                                                      burgdorferi
                   34.7%; Score 623.5; DB 4 69.5%; Pred. No. 3.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GAAELEKLFKAVENLSKAAQDTLKNA 177
                                      DB 4;
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  Indels
                                    Length
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1;
Gaps
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US-08-158-353-3
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAITOLL, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Padula
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C STREET: Two Militia Drive
180 ELTSPIV 186
                                        137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
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                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                           IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                                                                          IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
                                   KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                  KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
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                                                                                                                                                                                                                                                                                                                                                               210 amino acids
                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                   single
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Methods for Diagnosing Early
Disease
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                                                                                                                                                                                                            Score 623.5; DB 1;
Pred. No. 3.6e-42;
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US-08-235-836C-30
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS LENGTH: 210 amino action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
                                                                137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
197
                              180 ELTSPIV 186
                                                                               120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLEKAVENLSKAAQDTLKNAVK 179
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nes 129; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Upton
STATE: NY
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ELTSPVV
                                                            KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                         IGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
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203
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                                                                                                                                                                                                                                                                      34.4%; Score 617.5; DB 4 69.0%; Pred. No. 1.1e-41;
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                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                    DB 4;
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RESULT 8
US-08-209-603E-15
; Sequence 15, Application US/08209603E

Patent No.

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; PUBLICATION INFORMATION:
US-08-209-603E-15
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Best Local S
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TELEPHONE: (212) 657-335
TELEPAS: (212) 557-5635
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/0228:
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
FILING DATE: 19-JUN-1992
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MEDIUM TYPE: 3.5° FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                     LIBRARY: DSM 5662
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-JUN-1992 ATTORNEY/AGENT INFORMATION:
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120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
                                                   77
                                                                                 61
                                                                                                                17
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: ROBINSON, WILLIAM R. REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                             TYPE: AMINO ACID
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                                                                                 IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                                 IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
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                                                                                                                                                                            Conservative
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CHECK, ERWIN
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                                                                                                                                                                                           34.3%; Score 616.5; DB 4 69.0%; Pred. No. 1.3e-41;
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                                                                                                                                                                                                                                                                         amino acid analysis N/A
                                                                                                                                                                            24; Mismatches
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                                                                                                                                                                                                          DB 4;
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RESULT 10 US-08-031-295-2 ; Sequence 2, Ap

Application US/08031295

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                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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 197
                178 VKELTSPIV 186
                                                                              118 TNKLKSEHAVIGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                            137 TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0
                                                                                                                                                                                   STREET: Two Mil:
CITY: Lexington
                                                                                                                        77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                                       60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEF 117
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilton, Brook, STREET: Two Militia Drive
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VKELTSPVV 205
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Methods
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                                                                                                                                                                                                                                                 Score 588.5; DB 1;
Pred. No. 2.1e-39;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                               DB 1;
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RESULT 11
US-07-903-580-2
; Sequence 2, Application US/07903580
; Patent No. 6221363
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                                                                                                                                                                                                                                                                                                                                                                                      st Local Similarity tches 127; Conserv
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LENGTH: 212 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                  197
                                                                                                                                 178 VKELTSPIV 186
                                                                                                                                                                          137 TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                                                                                                       118
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NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/824,161 FILING DATE: 22-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,580
FILING DATE: 25-JUN-1992
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSE: Foley & Lardnor
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
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APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND
TITLE OF INVENTION: PREVENTION
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                                                                                                                                                                                                                                                       77
                                                                                                                                                                                                                                                                60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNE-ELKEKIDTAKQCSTEF 117
                                                                                                                                                                                                                                                                                                             17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                 1 MACNNSGKDG-NASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                VKELTSPVV 205
                                                                                                                                                                                                        TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                                                                                                                                                                                          AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
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11-JUL-1991
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US-08-235-836C-34
; Sequence 34, Application US/08235836C; Patent No. 6248562; GENERAL INFORMATION:
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                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,580
                                                                                                                                                 178 VKELTSPIV 186
                                                                                                                                                                                                  137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                            197 VKELTSPVV 205
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APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                          77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                           TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                                                                                              TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                                                                                                                                                                                                               AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                                                                                                                                                                                                                                                                                                       ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
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Pred. No. 4.3e-39;
3; Mismatches 36;
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APPLICANT:

Dunn, John J. Luft, Benjamin J.

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US-09-196-293-11
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Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                         Sequence 11, Application US/09196293 Patent No. 6183755
                                                                                                                                                                                        GENERAL INFORMATION:
               APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Motz, Manfred
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738 001US2
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EILING DATE: 29-APK-133-
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US
APPLICATION NUMBER: US
APPLICATION OD-111-93
TTYMG DATE: 01-112-93
CURRENT APPLICATION NUMBER: US/09/196,293
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MBrgaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL93-28A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                     197 VKELTSPVV 205
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MACNNSGKDG-NASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATK :59
                                                                                                                                                                                                                                                                                                                                                                            VKELTSPIV 186
                                                                                                                                                                                                                                                                                                                                                                                                                     TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS 196
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11973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.5%; Score 583.5; DB 4; Length 212; 68.3%; Pred. No. 5.1e-39; tive 21; Mismatches 36; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 6248562el Chimeric Proteins Comprising
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-196-293-11
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EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER FILING DATE: 1990-12-21
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
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APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-WURSIC, VERA
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
NUMBER OF SEQUENCES: 15
APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994 CLASSIFICATION: 436 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/EP90/02282 FILING DATE: 21-DEC-1990
                                                                                                              OPERATING SYSTEM: MS-D
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
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                                                                                                                                                                                                                                   TRY: USA
10016
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                                                                                                                                                         MS-DOS Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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Pred. No. 1.3e-38;
""Amatches 38;
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APPLICATION NUMBER: US 0 FILING DATE: 19-JUN-1992 ATTORNEY/AGENT INFORMATION:

US 07/862,535

REGISTRATION NUMBER:

ROBINSON, WILLIAM R.

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US-08-235-836C-36
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; ORIGINAL SOURCE:
US-08-209-603E-11
                                                                                                                                                                                                                                                Sequence 36, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: PROTEIN
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
COUNTRY: USA
ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhave
                                                     CITY: Upton
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
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                                                                                                                                                                                                                                                                                                                                                                       197 VKELTSPVV 205
                                                                                                                                                                                                                                                                                                                                                                                                          178 VKELTSPIV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
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                                                                                                                         Brookhaven National Laboratory
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; MOLECULE TYPE:
US-08-235-836C-36
                                                                                                                                                                                                                                                       Best Local Similarity 62.6 Matches 117; Conservative
                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bogosian, Margaret C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET MUMBER: BNL9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPAX: (516) 282-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION:
                                                               134
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
194 ELTNPVV 200
                              180 ELTSPIV 186
                                                                                             120
                                                                                                                            74
                                                                                                                                      61 IGKKIGNNG-LEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEETN 119
                                                                                                                                                                                          17
                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                          KLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAALTNSVK 193
                                                                         KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                       IGKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSEKFTT 133
                                                                                                                                                                                                                                                                                                                                                                                    amino acids
                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                       31.3%;
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                                                                                                                                                                                                                                                  ; Score 563; DB 4; Length 20
; Pred. No. 2e-37;
34; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                   4; Length 207;
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Search completed: March 18, 2002, 09:55:35 Job time: 348 sec THIS PAGE BLANK (USPTO)

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                       Score
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1797
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1: /cgn2_6/ptodata/2/paa/VGCTUS_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

9: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

10: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

12: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/US09_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/US09_COMB.pep:*

15: /cgn2_6/ptodata/2/paa/US09_COMB.pep:*

16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*

17: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*

18: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

19: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

21: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

22: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

23: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

24: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

25: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

26: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

27: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

28: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

29: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*

21: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
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Match Length DB
     100.0
100.0
99.6
99.6
85.6
85.1
85.1
85.1
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Gapop 10.0 , Gapext 0.5
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1797
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164.485 Million cell updates/sec
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US-09-596-746A-38
US-09-596-746A-78
US-09-596-746A-76
US-09-596-746A-42
US-09-596-746-42
US-09-596-746-74
US-09-596-746A-74
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ALIGNMENTS

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1154.5	1157.5	1162.5	1167.5	1167.5	1169.5	1169.5	1172	1172	1172.5	1173.5	1173.5	1176.5	1177.5	1178	1178	1181.5	1217	1217	1219.5	1219.5	1220	1221	1221	1224	1225	1225.5	1225.5	1229	1476	1476	1479	1482.5	1482.5	1484	1485.5
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19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19
-09-596	-09-596-746-5	-09-596	-09-596-746A-	-09-596-746-5	-09-596-	-09-596	-09-596	-09-596		US-09-596-746A-60	US-09-596-746-60	US-09-596-746-24	US-09-596-746A-34	US-09-596-746A-28	US-09-596-746-28	US-09-596-746A-24	US-09-596-746A-66	US-09-596-746-66	US-09-596-746A-82	US-09-596-746-82	US-09-596-746-36	US-09-596-746A-62	US-09-596-746-62	US-09-596-746-26	US-09-596-746A-36	US-09-596-746A-30	US-09-596-746-30	-09-	-09-596	-09-596	US-09-596-746-32	-09-596-	-09-596-746-7	-09-596-746A-	746-4
e 78,	56,	56,	52,	52,	64,	64,	,08	80,	34,	60,	60,	24,	34,	28,	e 28,		66,	66,	82,	82,	36,	62,	62,	26,	36,	30,	30,	26,	, 89	68,	Ø	e 72,	e 72,	e 32,	Sequence 40, Appl

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OTHER INFORMATION: OspC Chimera
US-09-596-746A-38
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Best Local Similarity
Matches 368; Conserv
                                                                                                                                                                                                                                                                                                                 SOFTWARE: 1
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38, Application US/09596746A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
                                                                                                                                                                                                                                                                  LENGTH: 368
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
181 LTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDE
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                                  IKSEHAVLGLDNITDDNAQRAIIKKHANKDKGAAELEKLFKAVENISKAAQDTIKNAVKE
                                                                                NAVKELTS 368
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                Score 1797; DB 19;
Pred. No. 1.4e-124;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                         Cause Lyme Disease in Humans
                                                                                                                                                                               Indels
                                                                                                                                                                                                     Length 368;
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Huma
FILLE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-66-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 391
TYPE: PRI
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; Sequence 76, Application US/09596746
; GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 366; Conservative
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APPLICANT:
385
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                                                                                      ATKAIGKKIGNNGLEANQSKNTSLLSGAVAISDLIAEKLNVLKNEELKEKIDTAKQCSTE 301
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AVKELTS 391
                                                                                                                                                                                                ATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTE
                                                                                                                                                                                                                                                                                                     TSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDEL
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Pred. No. 6.1e-124;
1; Mismatches 0;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Dise
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT ETLING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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Best Local S
Matches 366
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                                                                                                                                                                                                                             Sequence 42, Application US/09596746A GENERAL INFORMATION:
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EQ ID NO 76
LENGTH: 392
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CURRENT APPLICATION NUMBER: US/09/596,746A

CURRENT FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR APPLICATION NUMBER: US 60/140,042

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 392;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Danial
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42
TENGTH: 367
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; OTHER INFORMATION: OSPC Chimera US-09-596-746A-42
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                                                                                                                                                                                                                                                                                                                                                                  US-09-596-746-42
                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/09596746 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 319; Conserv
OTHER INFORMATION: OSPC Chimera -09-596-746-42
                                       LENGTH: 367
TYPE: PRT
ORGANISM: Artificial Sequence
                            FEATURE:
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86.7%;
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Pred. No. 2.1e-105;
20; Mismatches 27;
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Query Match

85.3%;

Score 1533;

DB 19;

Length 367;

Best Loc Matches

Local

al Similarity 318; Conser

Conservative

86.6%;

Pred. No. 4.9e-105;
0; Mismatches 27;

Indels

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Gaps

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; ORGANISM: OSPC
US-09-596-746-74
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US-09-596-746-74
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Matches 317
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                                                                                                                                                                                                                                                     SOFTWARE: Fa
EQ ID NO 74
LENGTH: 391
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4
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APPLICANT:
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  145
           122 KSEHAVLGLDNUTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL 181
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                                                                                                                                                   al Similarity 86.4 317; Conservative
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Seinost, Gerald
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                                                                                                                                                  85.1%; Score 1530; DB 19;
86.4%; Pred. No. 8.9e-105;
tive 21; Mismatches 27;
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; SOFTWARE: FastSEQ for W
; SEQ ID NO 74
; LENGTH: 392
; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746A-74
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US-09-596-746A-74
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Matches 317; Conservat
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Best Local
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
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386
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Seinost, Gera
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for Windows
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erald
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                                                                                                                                                                                                                                                                                                                                                            Score 1530; DB 19;
Pred. No. 8.9e-105;
1; Mismatches 27;
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Geraid
APPLICANT: Seinost, Geraid
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 369
TYPE: PRT
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US-09-596-746-40
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Best Local Similarity 84.3
Matches 312; Conservative
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                                                                                                                                  Sequence 40, Application US/09596746 GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhulzen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
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84.3%; Pred. No. 6.9e-102;
tive 24; Mismatches 31;
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US-09-596-746A-32; Sequence 32, Application US/09596746A; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
                                                                          CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 84 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 32 LENGTH: 370
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Best Local
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dattwyler, Raymond J. APPLICANT: Seinost, Gerald APPLICANT: Dykhuizen, Danial
                  LENGTH: 370
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: OspC Chimera
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Pred. No. 1.6e-101;
24; Mismatches 31;
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US-09-596-746A-32

82.6%; Score 1484; DB 19; 83.8%; Pred. No. 2.1e-101;

Length

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GENDANCE

APPLICANT: Dally.

APPLICANT: Seinost, Gerald

APPLICANT: Dykhuizen, Danilal

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki

TITLE OF INVENTION: Groups of Borrelia burgdorferi and

TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Disease in H

FILE REFERENCE: 2631.102-001

CURRENT APPLICATION NUMBER: US/09/596,746

CURRENT FILING DATE: 2000-06-16

PRIOR APPLICATION UNMBER: US 50/140,042

PRIOR FILING DATE: 1999-66-18

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 72

LENGTH: 392
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                                                                                                          Query Match
Best Local Similarity
Matches 310; Conserv
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Best Local Similarity 83.8
Matches 311; Conservative
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                                                                                                            82.5%; Score 1482.5; DB 19
84.0%; Pred. No. 2.9e-101;
vative 25; Mismatches 31;
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SOFTWARE: FastSEQ for
SEQ ID NO 72
LENGTH: 393
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APPLICANT: Dattwyler, Raymond J.
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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
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                           TEFTIKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTL 359
                                                        ATKAIGKKIGNN-GLEANQSKNTSLLSGAYAISDLIAEKLNVLKNE-ELKEKIDTAKQCS 299
                                                                                                                                      TSPIVHGNNSKKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDEL
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Maria J.C. Gomes-Solecki
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Seinost, Gerald
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US-09-596-746-32
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                                                                                    RESULT 15
US-09-596-746-68
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Sequence 68, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
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Best Local Similarity
Matches 310; Conserva
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SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelli That Cause Lyme Disease FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 199-06-18
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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                                                                                                                                                                                   LKNAVKELTS 368
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83.8%; Pred. No. 4.9e-101;
htive 25; Mismatches 31;
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US-09-596-746-68
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SEQ ID NO 68
LENGTH: 393
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Best Local Similarity 83.9
Matches 309; Conservative
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
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TYPE: PRT
359 LKNAVKELTS
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384 LKNAVKELTS
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83.5%; Pred. No. 8.9e-101;
tive 26; Mismatches 31;
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Search completed: March Job time: 973 sec 18, 2002, 10:08:45

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Minimum DB seq
Maximum DB seq
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Perfect score:
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1: /cgn2_6/ptcdata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*
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US-09-974-992-5
US-09-974-992-3
US-09-915-242-5883
US-09-815-242-13080
US-10-072-851-13080
US-10-072-851-13080
US-10-072-851-12996
US-10-072-851-12996
US-10-072-851-12996
US-10-072-851-15596
US-10-072-851-12913
US-09-815-242-12913
US-09-815-242-13013
US-09-815-242-13013
US-09-708-427-15046
US-09-708-427-13028
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e 12996, A
e 12996, A
e 12913, A
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e 12913, A
e 12913, A
e 15044, A
e 13228, A
e 13228, A
e 13228, A
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ALIGNMENTS

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RESULT 1
US-09-974-92-7
US-09-974-92-7
Sequence 7, Application US/09974992
Sequence 7, Application US/09974992
GENERAL INFORMATION:
APPLICANT: Mathiesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
FILE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CUURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
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; ORGANISM: Borrelia afzelii
US-09-974-992-7
RESULT 2
US-09-974-992-5
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Best Local S
Matches 130
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                                                                                            178 VKELTSPIV 186
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Local Similarity 68.8%; Pred. No. 2.9e-32;
nes 130; Conservative 20; Mismatches 36;
                                                                                                                                                                 TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                                                                                                                                            TNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNS
                                                                       VKELTSPVV 205
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; ORGANISM: Borrelia garinii
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       Query Match
Best Local Similarity
Matches 118; Conserv
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PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09974992 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          *APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: NOVEL OSPC-derived peptide fragments
FILE REFERENCE: 459-666P
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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SEQ ID NO 5
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/180,089 PRIOR FILING DATE: 1999-05-13
                                                                                                                           LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mathiesen, Marianne J.
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
COMMENT OF SEQ ID NOS: 40
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TYPE: PRT
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 32.4%; Score 583; DB 6; Local Similarity 67.5%; Pred. No. 6.8e-32; Pes 129; Conservative 24; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSTKLKDNHAQLGIQGVTDENAKKAILKANAAGKDKGVEELEKLSGSLESLSKAAKEMLA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTNKLKSEHAVLGLDNLTDDNAQRAILKKH-ANKDKGAAELEKLFKAVENLSKAAQDTLK 175
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        Conservative
                     31.6%;
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       33;
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Score 567; DB b; Pred. No. 7.6e-31; ""amatches 32;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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US-09-815-242-5883
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SEQ ID NO 5883
LENGTH: 837
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Best Local :
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-10-23
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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218 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 272
                                       110 AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                           100 NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 159
                                                                                        160
                                                                                                                 54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                                                                                                   4 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI----
                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IGKKIGNNG-LEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
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                                                                             DSIANEAT-IKAGONYTDASONKOTDYNSAVTAAKAIIGOTTSPSMNAQEINQAKDOV-T
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
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                                                                                                                                                                                                                                               84;
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Pred. No. 3.8e-05;
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NLS--KAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESN 222

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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5883
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 837
TYPE: PRIT
ORGANISM: Staphylococcus aureus
-10-072-851-5883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITRA.028A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT FILING DATE: 2002-02-08 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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 AVVLAVKEVETLL-----ASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDL
                                                                                                                                                                                        DSTANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVVLAVKEVETLL-----ASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDL
                                                    NADALNTAMTNLKNGIQD-----QNTIKQG-VNFTDADEA---
                                                                       NLS--KAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESN
                                                                                                                    AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN
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                                                                                                                                                      AKQCSTEFTNKLK - - - - - SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE
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Ohlsen, Kari L.
Zyskind, Judith W.
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Yamamoto, Robert
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US-09-815-242-13080
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SEQ ID NO 13080
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
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PRIOR APPLICATION NUMBER: 60/207,727
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AVVLAVKEVETLL------ASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDL
                                                NADALNTAMTNLKNGIQD------QNTIKQG-VNFTDADEA---
                                                                      NLS--KAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESN 222
                                                                                                                                                      AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE
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                                                                                                                    AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI----EGATHVNEVTQAQN
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Trawick, John D.
Carr, Grant J.
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Zyskind, Judi
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                                                                                                                                                                                                                                                                                                                                             Score 191; DB 6
Pred. No. 4e-05;
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FILE REFERENCE: ELITRA.026A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13080
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В
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Best Local Similarity
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TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
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TYPE: PRT
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   407 TS--INNAQKEALKSQIEGATTVAGVNQVSTTASELNTAMSN------LQNGINDE
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                                                                                                                                                                                  NLS--KAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESN 222
                                                                                                                                                                                                                                                                 AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE
                                                                                                                                                                                                                                                                                                    DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
                                     IAEKLNVLKNEELKEKID-------TAKQCSTEFTNKLKSEHAVLGLDN-LTDD
                                                                            AYTNAVTQAEQILNKAQGPNTSKIJGVETALENVQRAKNELNGNQNVANAKTTAKNALNNL
                                                                                                             AVVLAVKEVETLL------ASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDL
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Zyskind, Judith W.
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Zamudio, Carlos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         84;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 191; DB /; Pred. No. 4e-05; Pred. No. 4e-18; Indels
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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SEQ ID NO 5835
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                       224 VYLAVKEVETLLASI-----DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLI--
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       998 VSTTASELNTAMSNLQNGINDEAATKAAQKY----TDADREKQTAYNDAVTAAKTLLDK 1052
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                                                                                                                                                                                          KLFKAVENLSKAAQD--TLK--------NAVKELTSPI--VHGNNSRKD-- 194
                                                                                                                                                                                                                                                                                                        DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
                                                                                                                                                       ALNTAMTNIKNGIQDQNTIKQGVNFTDADEAKRNAYTNAVTQAEQIINKAQGPNTSKDGV 937
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Zyskind, Judith W.
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RESULT 9
US-10-072-851-5835
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 5835
LENGTH: 2434
TYPE: PRT
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best Local Similarity 22.2
Matches 107; Conservative
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TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                       4 NNSGKDGNASANSADE---SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI---- 53
KLFKAVENLSKAAQD--TLK-------NAVKELTSPI--VHGNNSRKD--
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                                                                ETALENVQRAKNELNGNQNVANAKTTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQ
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Boone, Charles
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Zyskind, Judith W.
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Yamamoto, Robert T.
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Zamudio, Carlos
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Pred. No. 0.00057;
31; Mismatches 161
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US-09-815-242-12996
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US-09-815-242-12996
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SEQ ID NO 12996
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: 'Xu, H. Howard TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308
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  158 KLFKAVENLSKAAQD--TLK----
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                                                                AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQIEGATHVNEVTQAQNNAD 1656
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FILING DATE: 2001-03-21
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Zyskind, Judith W.
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Pred. No. 0.0019;
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  NAVKELTSPI--VHGNNSRKD--
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Best Local Similarity
Matches 107; Conserv
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TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA, 028A
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PRIOR APPLICATION NUMBER: 60/257,636
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15811
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                  1599 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQIEGATHVNEVTQAQNNAD 1656
                                                                                1541 DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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                                                  110 AKOCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKK-----HANK-DKGAAELE 157
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Boone, Charles
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Zamudio, Carlos
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; Pred. No. 0.0019;
81; Mismatches 161; Indels 13
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SEQ ID NO 7646
LENCTH: 1881
TYPE: PRT
ORGANISM: Candida albicans
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Best Local Similarity
Matches 112; Conserv
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CURRENT FILING DATE: 2001-12-20
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APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
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NAME/KEY: MISC_FEATURE
LOCATION: (1881)..(1881)
OTHER INFORMATION: x-any amino acid
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1682 KOLEELEKVKSDLQTADEKLKGITEREIALK--
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APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies
FILE REFERENCE: 10182-005-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 VETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLI---AEKLNVLKNEE 102
                                                                                                                                                                                            --ANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNS---
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                                                                                                                             SIEEKNNQIKELSETIKSLKTELKTSGDALKQSQKEY-----KTLKTKNSDTESKLE 1681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESGTTVAGVQGIQANAGTLDQAMNQLRQSIASKD-ATKSSEDYQDANADLQNAYNDAVTN 1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALNTAMTNLKNGIQDQNTIKQGVNFTDADEAKRNAYTNAVTQAEQILNKAQGPNTSKDGV 1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSEHAVLGLDNL----TDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSTTASELNTAMSNLQNGINDEAATKAAQKY-----TDADREKQTAYNDAVTAAKTLLDK 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETALENVQRAKNELNGNQNVANAKTTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQ 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AEKLNVLK-----NEELKEKIDTAKQ------CSTEFTNKL 306
                                                              -ADESVKGPNLTEISKKITESNAVVLAVKEVETL----LASIDELA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.7%; Score 173.5; DB 7; 25.6%; Pred. No. 0.0015; tive 55; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NAVKELTSPI -- VHGNNSRKD-- 194
SELETYKNSGLSTTSELA 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for Drug Target Discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1881;
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LOCATION: (1881)..(1881)

OTHER INFORMATION: X=any amino acid

US-10-072-851-15590
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 15590
LENGTH: 1881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Prolliferation FILE REFERENCE: ELITRA.028A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Candida albicans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1731 -- ALTKTV--KSLE-KEKEELQFLSGNKSKELEDYIQKHSDISEKLKAL-TDELKEKTKQ 1784
                                                                                                                                                                                                   1524 IVTLQTELKDRISEVEKER-----AMLSENSETVIKEY--SDKIKSLESKINSIKENH 1574
                                                                                                                                                                                                                                                                                 1470 ALTKSSKDLEVCGNQKSELQDSLKSVKSELKNFENKYNQETTSLKDEIEEKQ-----KE
                                     1630 SIEEKNNQIKELSETIKSLKTELKTSGDALKQSQKEY-----KTLKTKNSDTESKLE 1681
                                                                                                                                                       103 LKEKIDTAKQCSTEFTNKLKSEHAVLGLDN-----LTDDNAQ----RAILKKH----- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 LSKAAQDTLKNAVKELTS 368
  202
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                                                                                                                                                                                                                                                                                                                                                            Whatch 9.7%; Score 173.5; DB Local Similarity 25.6%; Pred. No. 0.0015; Pred. No. 0.0015; Mismatches 1:
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                                                                                                                                                                                                                                                                                                                        ACNNSGKD----GNASANSAD--ESVK------GPNLTEISKKITESNAVVLAVKE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDDSKKKLTELENDLTSTK-----KELETEKTQTSKFKNLEERKDKEIVKLNKELELLKN 1839
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                                                                             --ANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIVHGNNSRKDGNASTNS---
                                                                                                                   SKE-ITTHNEQKT----SLKQDIAKLSQDHESAQTQLEDKENQLKELKASLEKHNTESAT 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bussey, Howard
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Zamudio, Carlos
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--ADESVKGPNLTEISKKITESNAVVLAVKEVETL----LASIDELA 242
                                                                                                                                                                                                                                                                                                                                                                  55; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 1881
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1132 TAKKQEINQNTNATTEEKQVALNQVDQELATAINNINQADTNAEVDQAQQLGTKAINAIQ 1191

20 SVKGPNLTEISKKITESNAVVL--AVKEVETLLASIDELATKA---IGKKIGNNGLEA-- 72

Indels 87; Gaps

14;

Conservative

1192 PNIVKKPAALAQINQHYNAKLAEINATPDATNDEKNAAINTL-NQDRQQAIESIKQAN-- 1248

-NQSKNTSLL---SGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTE 116

FTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKN 176

-TNAEVDQAATVAENNI--DAVQVDVVKKQAARDKITAEVAKRIEAVKQTPNATDEEKQA 1305

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177 AVKELTS---

-- PIVHGNNSRKDGNASTN--

-SADESVKGPNLTEISKKITES 221

1249

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; ORGANISM: Staphylococcus aureus US-09-815-242-5815
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/21,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5815
Query Match
Best Local Similarity
Matches 85; Conserv
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                           LENGTH:
TYPE: PF
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                                                                                                                                                                                                  2076
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9.5%; Score 171.5; DB 6; 20.0%; Pred. No. 0.0023; ative 78; Mismatches 174;
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5815
LENGTH: 2076
                                                                                                                                                                                                                                                                                                                                           Query Match 9.5%;
Best Local Similarity 20.0%;
Matches 85; Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITRA.028A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Staphylococcus aureus
10-072-851-5815
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1306 AVNQINQLKDQAINQINQNQTNDQVDTTTNQAVNAIDNVEAEVVIKPKAIADIEKAVKEK 1365
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                                                                                  1249 -TNAEVDQAATVAENNI--DAVQVDVVKKQAARDKITÄEVAKRIEAVKQTPNATDEEKQA 1305
                                                                                                                                                                      1192 PNIVKKPAALAQINQHYNAKLAEINATPDATNDEKNAAINTL-NQDRQQAIESIKQAN-- 1248
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                                        177 AVKELTS-----PIVHGNNSRKDGNASTN-----SADESVKGPNLTEISKKITES 221
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Zyskind, Judith W.
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Zamudio, Carlos
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Search completed: March 18, 2002, 09:58:28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 19-209 <LIV>
A;Cross-references: EMBL:L42894; NID:g858722; PIDN:AAB37002.1; PID:g1695219
A;Experimental source: strain 28691
C;Genetics:
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A;Residues: 1-211 <RES>
A;Cross-references: EMBL:U04282; NID:g2314881; PIDN:AAC45540.1; PID:g434666
C;Genetics:
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Outer surface protein C - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-reb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
C;Accession: S70287
R;Livey, I; Gibbs, C.P.; Schuster, R.; Dorner, F.
MOI. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation
A;Reference number: S70285; MUID:96296448
A;Accession: S70287
                                                                                                                                                                                                                A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-193 <LIV>
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evenson, B.; Bartl
Microbiol. Lett.
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                                      60 AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFT 118
                      77 AIGKKIHONNGIDTENNHNGSLLAGAYAISTLITOKLGGLKNEELKEKIAAVKKCSEEFT
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                                                                                               1 MACNNSGKDGN-ASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKK
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                                                                              ISCNNSGKDGNAASTNPADESVKGPNLTEISKKITDSNAVVLAVKEVGALLTSIDELATK 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSPIV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTBETNK 120
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                                                                                                                                                             35.9%;
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                                                                                                                                                 18;
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                                                                                                                                             Score 646; DB 2;
Pred. No. 1.2e-23;
8; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 661; DB
Pred. No. 2.3e
20; Mismatches
                                                                                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
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                                                                                                                                                                       Length 211;
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                                                                                                                                            Indels
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                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                      North American
                                                                                                                                         Gaps
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Best Local S
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-191 <RES>
                                                                                                                                                                          outer surface protein C - Lyme disease spirochete (fragment) (Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C:Accession: 140.153 #Sequence_revision J.M.; Steere, A.C. Infect. Immun. 62, 3213-3221, 1994
       A;Gene: ospC
C;Superfamily:
                                                 A;Cross-references: EMBL:U08284; NID:g469561; PIDN:AAA21460.1;
                                                                                                                             A;Title: Humoral immune response to outer A;Reference number: I40153; MUID:94314437 A;Accession: I40153
                                                                                                                                                                                                                                                                                                  I40153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outer surface protein C - Lyme disease spirochete (:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change c:Accession: S70279 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:L42898; NID:g858729; A;Experimental source: strain 25015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-193 <LIV>
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A;Accession: S70279
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                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown
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Best Local S
Matches 135
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                                                                                                                                                                                                                                                                                                                                                                      LTSPVV
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         Lyme
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     disease spirochete
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Pred. No. 1.7e
16; Mismatches
surface protein
                                                                                                                                                             surface protein
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L.7e-23;
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                                                     PID: 9469562
                                                                                                                                                           Borrelia burgdorferi i
                                                                                                                                                                                                                                 26-May-2000
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Similarity

35.6%; 73.9%;

Score Pred.

No. 2

DB 2; .3e-23;

Length

191;

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A;Cross-references: EMBL:x69596; NID:g311391; PIDN:CAA49306.1; R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in Osp A;Reference number: S70255; MUID:96296448
A;Accession: S70281
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, Med. Microbiol. Immunol. 182, 37-50, 1993
A-Title: Genetic heterogenity of the genes coding for the outer surface protein C prerence number: S37726; MUID:93268136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Fukunaga, M.; Hamase, A.
7. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence analysis A;Reference number: 140269; MUID:96025162
A;Accession: I40269
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          er surface protein C - Lyme disease spirochete
pecles: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000
C;Accession: G70218; I40269; S37726; S70281
C;Accession: G70218; I40269; S37726; S70281
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
BOWMEN, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
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                                                                                                                     A; Experimental source: strain C; Genetics:
                                                                                                                                                         A;Molecule type: DNA
A;Residues: 19-210 <LIV>
A;Cross-references: EMBL:L42887; NID:g858715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-210 <KLE>
A;Cross-references: GB:AE000792; NID:g3253098; PIDN:AAC66329.1; PID:g2689901;
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A70100; MUID:98065943
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                                                                               A; Gene: ospC
C; Superfamily:
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A; Residues: 1-210 <JAU>
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A; Residues: 1-210 < RES>
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A;Status: nucleic acid sequence not shown;
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  Local Similarity
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                                                                           disease spirochete surface
34.7%;
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Score 623.5; DB 2; Pred. No. 1.3e-22;
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                                                                                                                                                             PIDN: AAB36995.1;
                                                                               protein
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                    210;
                                                                                                                                                           PID:g1695212
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outer surface protein C precursor - Lyme disease spirochete (strain C;Species: Borrelia burgdorferi (Lyme disease spirochete)
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A;Molecule type: DNA
A;Residues: 1-50, 'E', 52-61, 'I', 63-117, 'D', 119-122, 'V', 124-173, 'D', 175-176, 'D', 178-209
A;Cross-references: EMBL:X83555; NID:g872019; PIDN:CAA58545.1; PID:g872020
C;Superfamily: Lyme disease spirochete surface protein C
E;1-18/Domain: signal sequence #status predicted <SIG>
E;19-209/Product: outer surface protein C #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outer surface protein C precursor - Lyme disease spirochete (strain B. pacificus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, January A; Reference number: S72679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-209 <JAU>
A; Cross-references: EMBL: X83555
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                                                                                                      LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180
                                                                                                                                                                     IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNK 120
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LTSPVV
                                                                      LKNGNAQLGLAAATDDNAKAAILKTNGTNDKGAKELKELSESVESLVKAAQVMLTNSVKE
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                                                                                                                                                 IGQKIDANGLGVQANQNGSLLAGAYAISTLITQKLSALNSEELKEKIAKVKKCSEDFTNK
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Outer surface protein C - Lyme disease spirochete C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_c:Accession: $70286  
R;Livey, I:, Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
A:Title: Evidence for lateral transfer and recombination: A;Reference number: $70255; MUID:96296448
A:Accession: $70286
A:Status: nucleic acid sequence not shown
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                                                                                                                             A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface
                                                                                                                                                                                    A;Cross-references: EMBL:L42897; NID:g858728; PIDN:AAB37006.1; PID:g1695222
A;Experimental source: strain 26815
                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-193 <LIV>
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A:Accession: $72669
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C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-210 <JAU>
A; Cross-references: EMBL: X69589
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sidues: 1-124,'D',126-139,'E',141-210
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                                                                          Local
              3 CNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIG
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                                                                                            Match
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les 129; Conserv
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                                                                        Similarity
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                                                     Score 619; DB 2
Pred. No. 2e-22;
2; Mismatches
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Pred. No. 2.1e-22;
Pred. No. 2.32;
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outer surface protein C precursor - Borrelia afzelii (strain PLj7)
C:Species: Borrelia afzelii
A:Variety: strain PLj7
C:Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
C:Accession: S69922; S72675
R:Jauris-Heipke, S:; Liegl, G.; Preac-Mursic, V.; Roessler, D.; Schwab, E.; S
J. Clin. Microbiol. 33, 1860-1866, 1995
A:Title: Molecular analysis of genes encoding outer surface protein C (OspC)
A:Reference number: I40047; MUID:95395018
A:Accession: S69922
A; Molecule type: DNA
A; Residues: 1-212 <JAU>
                                      A; Status: nucleic acid sequence not shown
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C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
C;Accession: S70284
R;Livey, I; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation in A;Reference number: S70255; MUID:96296448
A;Accession: S70284
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A; Residues: 1-191 <LIV>
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Best Local Similarity
Matches 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPIV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEE-LKEKIDTAKQCSTEFTNKL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNNSGKDGNASTNSADESYKGPNLTEISKKITESNAVVLAVKEVAALLSSIDELA-KAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:L42896; NID:g858724; PIDN:AAB37004.1; PID:g1695221
ce: strain 27579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%; Score 614; DB 2; 69.6%; Pred. No. 3.3e-22;
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                                                                                                                                                             Soutschek
                                                                                                              of Borre
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181 ELTNPVV

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outer surface protein C - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_C; Accession: S70268
R; Livey, I; Gibbs, C.P.; Schuster, R; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A; Title: Evidence for lateral transfer and recombination:
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C;Superfamily: Lyme disease spirochete surface protein
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A;ResIdues: 1-125,'V',127-154,'E',156-212 <ROB
A;Cross-references: EMBL:X81523; NID:g804956;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A; Reference number: S72674 A; Accession: S72675
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A; Accession: $70268
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A; Residues: 1-194 <LIV>
                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                 ;Superfamily:
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Best Local :
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Best Local :
             180
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Local Similarity . 69.3%;
                                                                                           61
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                                                                                                                                                                       w
                                                                                                                                          ELTSPIV 186
                                     KLKGGHAELGLAAATDENAKKAILKTNGTKDKGAEELEKLFKSVESLAKAAKESLINSVK
                                                   KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                         GKKIQNNGLTAEQNQNGSLLAGAYAISALITKKLDELTKNSGELKGEVEKAKKCSEEFTN 120
                                                                                                       GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVL-KNE-ELKEKIDTAKQCSTEFTN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKELTSPIV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TINKLKGGHAELGLAAATDDNAKKAILKTNGTKDKGAEELEKLFKSVESLAKAAKESLTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
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                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                 disease spirochete surface
                                                                                                                                                                                                            33.7%; Score 605.5; 69.0%; Pred. No. 8.
                                                                                                                                                                                                27;
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                                                                                                                                                                                                                                                                                                                    NID:g858716;
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Pred. No. 4.4e-22;
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956; PIDN:CAA57243.1; PID:g804957
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R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.;
J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer surfl A; Reference number: I40104; MUID:95286481
A;Accession: I40104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RES>
A;Cross-references: EMBL:X84785: NTD...
                                                                                                                                                                                                                                                                                                                                                                                                                                                      outer surface protein C - Lyme disease spirochete (strain MUL) (fragment) (Species: Borrelia burgdorferi (Lyme disease spirochete) (C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-200 C;Accession: 140125; S54195  
R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; H. J. Bacteriol. 177, 3036-3044, 1995  
A;Title: Evolution of the Borrelia burgdorferi outer surface protein OspC A;Reference number: 140104; MUID:95286481
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I40104
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                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-178 <RES>
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C;Superfamily:
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Local Similarity
                                                                                                                                                              / Match 33.7%;
Local Similarity 73.0%;
nes 130; Conservative 1
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                                                                              LAVEAGHNGTSLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
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                                                                                                 LEANOSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEFTNKLKSEHAVL 128
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                                                                                                                                                                                                                                                Score 605; DB 2;
Pred. No. 7.9e-22;
9; Mismatches 27;
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Pred. No. 7
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A;Molecule type: DNA
A;Residues: 19-210 <LIV>
A;Cross-references: EMBL:L42893; NID:g858721; PIDN:AAB37001.1; PID:g1695218
A;Experimental source: strain 297
C;Genetics:
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R;Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer surface protein C A;Reference number: I40143; MUID:95154673
A;Accession: I40144
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
Search completed: March 18, 2002, 09:56:48 Job time: 371 sec
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C;Superfamily: Lyme disease spirochete surface protein C
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A;Accession: $70282
A;Status: nucleic acid sequence not shown
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Microbiol. 18, 257-269, 1995

Ay-Itle: Evidence for lateral transfer and recombination in OspC variation in Lyme disea
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A;Molecule type: DNA
A;Residues: 1-210 <RES>
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                                                                                                                                                                                                                                                                          119 NKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAAELEKLFKAVENLSKAAQDTLKNAV 178
                                                                                                                                        196 KELTSPVV 203
                                                                                                                                                                                        179 KELTSPIV 186
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Maximum Match 100%
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Bacteria; Spirochaeta
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PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA

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Pfam; PF01441; Lipoprotein_6; 1.

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Outer membrane; Lipoprotein; Signal; Plasmid; Antigen SIGNAL

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Best Local S
Matches 82
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001800; Lipoprotein_6. pfam; pF01441; Lipoprotein_6; 1. proDom; pD001149; Lipoprotein_6; 1. pROSITE; pS00013; PROKAR_LIPOPROTEIN; 1. Outer membrane; Lipoprotein; Signal; Plasmid.
                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
VARIABLE MAJOR OUTER MEMBRANE LIPOPROTEIN 3 P
STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; Pubmed-1484486;
Restrepo B.I. Kitten T., Carter
"Subtelomeric expression regions
                                                                                                                                                                                                                                                         Q02448;
01-JUL-1993
                                                                                                                                                                                                                                                                                                                  BORHE
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Mol. Microbiol. 6:3299-3311(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Restrepo B.I., Kitten T., Carter C.J., Infante D., Barbour A.G.; "Subtelomeric expression regions of Borrelia hermsii linear plasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SSP. HS1 SEROTYPE 24;
MEDLINE=93133110; PubMed=1484486;
                                                                        SEQUENCE FROM N.A
                                                                                                                               Bacteria;
                                                                                                                                                  Plasmid
                                                                                                                                                                  Borrella hermsii.
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                                                                                                                                                                                       VMP3.
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N-ACYL DIGLYCERIDE
; F1583F510246F7C7
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C.J., Infante D., Barbour A. of Borrelia hermsii linear p
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CRC64;
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protein
J. Cell
[2]
                                                                        Nakajima H.,
Yamasaki M.;
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P25386;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO
USO1 OR INT1 OR YDL058W.
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Mol. Microbiol. 6:3299-3311(1992).
-i- FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
                                                                                                                                                         Saccharomycetales;
NCBI_TaxID=4932;
[1]
                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                             MEDLINE-91185402; Pu
Nakajima H., Hirata
                                                                                                                   SEQUENCE FROM N.A. STRAIN-X2180-1A;
                                     "A cytoskeleton-related gene, uso1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM ONE SURFACE EXPOS
SUBCELLULAR LOCATION:
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transport in Saccharomyc Biol. 113:245-260(1991).
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                                                                           PubMed=2010462;
ta A., Ogawa Y.,
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39.8%;
                     Saccharomyces cerevisiae.
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VARIABLE MAJOR OUTER MEMBRANE
LIPOPROTEIN 3.

N-ACYL DIGLYCERIDE (PROBABLE)
; 684C74D35F87C771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 311.5; DE
Pred. No. 4e-08;
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OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-
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E > K (IN REF. 2).
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                                                                                                                                                                                                                                              Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Digarder D., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Wardis E., Menezes S., Miller N., Nhan M., Pauley A., Pelusc Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilson R., Waldon R., Woldman P., Vaudin M., Wilson R., Waterston R., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: BSSENTIAL COMPONENT OF THE NUCLEOSKELETON. POTENTIAL COMPONENT OF THE NUCLEOSKELETON.
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20-AUG-2001
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"The NUF1 gene encodes an essential co
is a potential component of the yeast
j. Cell Biol. 116:1319-1332(1992).
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CT-1993 (Rel. 27, Last sequence update)
UG-2001 (Rel. 40, Last annotation update)
PROTEIN (SPINDLE POLY BODY SPACER PROTEIN
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an email to license@isb-sib.ch).
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CAGA, HELPJ STANDARD;

T 20-AUG-2001 (Rel. 40, Created)

T 20-AUG-2001 (Rel. 40, Last sequence update)

T 20-AUG-2001 (Rel. 40, Last annotation update)

T 20-AUG-2001 (Rel. 40, Last annotation update)

E CYTOTOXICITY ASSCIATED IMMUNODOMINANT ANTIGEN (12

DE (CAG PATHOGENICITY ISLAND PROTEIN 26).

GN CAGA OR CAI OR CAG26 OR JHP0495.

GN CAGA OR CAI OR CAG26 OR JHP0495.

OS Helicobacter pylori J99 (Campylobacter pylori J99)

OS Helicobacter Pylori J99 (Campylobacter pylori Helicobacter)
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PIR; S34288; S34288.
SGD; S0002764; NUF1.
Coiled coil; Nuclear
                                      Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria Nickelsen M., Milis D.M., II. Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
                                                                                           SEQUENCE FROM N.A. MEDLINE-99120557; PubMed-9923682;
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pathogen H
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Similarity 23.4%;
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e comparison of two unrelated Helicobacter pylori.";
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59 NU
731 NU
747 NU
944 AR
111781 MW;
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NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL NUCLEAR FOR THE NUCLEAR LOCALIZATION SIGNAL ARG/TYR-RICH.

MW; 04FAA074BBBAA0BC8 CRC64;
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Pred.
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Embryo;
MEDLINE-90349606; PubMed=2117279;
MEDLINE-90349606; PubMed=2117279;
Ketchum A.S., Stewart C.T., Stewart M., Kiehart u....
                                                                                                                                                                                                                                                MYSN_DROME
Q99323;
01-JUN-1994
01-JUN-1994
20-AUG-2001
MYOSIN HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as low
modified and this statement is not remove
entitles requires a license agreement (so
or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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FUNCTION: MAY BE NECESSARY FOR OR FUNCTION OF THE CYTOTOXIN.
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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Pred. No. 0.95;
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POLY-ASN.
POLY-B5E86B81CEBD0F2
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DOMAIN
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DOMAIN
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SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PFINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0005634; zip.
InterPro; IPR000048; IQ.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A36014; A36014.
PIR; B36014; B36014.
HSSP; P08799; IMND.
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                                                                                                                                                                                                                                                                                         Local Similarity
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IERARSELQEKCTK-LQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQQLLE-EET
                                                                                                                                                                                                                 VADLKEQLNERRVQVDEMQAQLAKREEELTQTLLRIDEESATKATAQKAQRELESQLAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR CELLULARIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                              TLKNAVKELTSPIVHGNNSRKDGNASTNSADESVKGPNLTEISKKITESNAVVLAVK--E
                                                                                                        TL-----KKSLEEETVNHEGVLADMRHKHSQELNSINDQLENLRKAKTVLEKAKG 1271
                                                                                                                                 VLGLDNLTDDNAQRAILKKHAN------KDKGAAELEKLFKAVENLSKA-----AQD 172
                                                                                                                                                           QEDIEAEKAARAK----AEKVRRDLSEELEALKNEILDSLDTTAAQ--QELRSKREQELA 1221
                                                                                                                                                                                     NNGLEANOSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKOCSTEFTNKLKSEHA 126
                                                                                                                                                                                                                                           LTEISKKITESNAVV-----LAVKEVE---TLLASIDELATKAIGKKIG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the 5' untranslated sequence."; tl. Acad. Sci. U.S.A. 87:6316-6320(1990)
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1303
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                                                                                                                                                                                                                                                                          Conservative
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859
2017
232
260
694
727
758
2017
1970
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                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                            WW;
                                                                                                                                                                                                                                                                       Score 162.5; D
Pred. No. 1.9;
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        ATP.
25 KDA/50 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING.
LIGHT MEROMYOSIN (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is not removed.
                                                                                                                                                                                                                                                                                                                                                    ALPHA-HELICAL TAILPIECE (LMM).
GLOBULAR TAILPIECE.
MISSING (IN SHORT ISOFORM).
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COILED
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                                                                                                                                                                                                                                                                                                                                          73E3CB02BA8F2528 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEAD-LIKE
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                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                       139;
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647 ISQITRESTEN--MSLLNKEIQDLYDSKSDISIK-LGKEKSSRILAEERFK---LLSNTL 700

26 LTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAY 85

Matches

96; Similarity

Conservative

08;

Mismatches

155;

Indels

119;

Gaps

18;

.4

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MLP1_YEAST
ID MLP1_YEAST
AC 002455
AC 002455
AC 002455
DT 01-0C1
DT 01-0C1
DT 01-0C1
DT 20-AUC
DE MYOSIN
GN MCD1_1
GN NCBL_1
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   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                           EMBL; L01992; AAA34783.1; -
EMBL; X73541; CAA51948.1; -
EMBL; Z788320; CAA82174.1; -
PIR; S38173; S38173;
SGD; S0001803; MLP1.
                                                                                                                                         DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q02455;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bou G.,
Remacha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerevisiae chromosome XI contains new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93247549; PubMed-8483450;
Koelling R., Nguyen T., Chen E.Y., Bo
"A new yeast gene with a myosin-like
Mol. Gen. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94205265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1428 ADLAKELEEGKKRLNKDIEALERQVKELIAQNDRLDKSKKKIQS 1471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994
20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :- SIMILARITY: SOME, TO THE TPR ONCOGENE.
:- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINCE FROM N.A. (Cantalejo J.G INE-94205265; PubMed-8154186; INE-94205265; PubMed-8154186; G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G Cha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J. Complete sequence of a 15,820 bp segment of Saccharomyces complete sequence and the UBI2 and MPL1 genes and the UBI2 and the UB
                                                                                                                                                                  d coil; DNA repair.
N 69 487
N 531 1678
N 1834 1866
ICT 301 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long and this statement is not removed.
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8.9%;
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Last annotation update)
                                                                                                                          COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
R -> A (IN REF. 1).
MW; 683A0D34C9066867 CRC64;
Score 159.5;
Pred. No. 2.4
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S., Revuelta J.L.;
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01-FEB-1994
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laissfer N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAEEL
             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                             This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058
                                                                                                                                            Durbin R.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                elegans
                                                                                                                                                                                                                                                                  Waterson R., Watson Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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T05G5.9.
                                                                                                                                                                                  REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
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39, Last sequence update)
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KDA PROTEIN T05G5 9 IN CH
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Caenorhabditis.
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Best Local
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Pfam; PP01465; GRIP; 1.
Hypothetical protein; Coiled c
DOMAIN 75 137
DOMAIN 160 509
DOMAIN 562 641
SEQUENCE 705 AA; 80637 MW;
                                                                                                                                                                                                                                                           Q00799;
01-APR-1993
01-APR-1993
01-OCT-1996
                        between
the Euro
                                                                                             Plasmodium vivax (stra Eukaryota; Alveolata; NCBI_TaxID=31273;
                                This SWISS-PROT entry is copyright. It is produced throughout the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z27079; PIR; S41009; S
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European Bioinformatics Institute.
                                                                     HUMAN RETICULOCYTE CELLS.
SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
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non-profit institution and this statement is
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(Rel. 25, Last sequence update)
(Rel. 34, Last annotation updat
BINDING PROTEIN 2 (FRAGMENT).
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Pred. No. 0.
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Best Local S
Matches 106
       STRAIN-CAMTON-S, AND OREGON-R; STRAIN-CAMTON-S, PubMed=1840513; Chi H.-C., Juminaga D., Wang S.Y., "Structure of the Drosophila gene DNA Cell Biol. 10:451-466(1991).
                                                                                                                           IMG1_DROME STANDARD; PRT; 1639 AA.

P15315; Q24373; Q3VT18;
01-APR-1990 (Rel. 14, Created)
101-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
1AMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN).

LANDININ GAMMA-1 CHAIN PRECURSOR (IAMININ B2 CHAIN).

LAND2 OR LAMC1 OR LAMG1 OR CG3322.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ebhydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hilbrids S., Ashburner M.A., Galle R.F.,
RA George R.A., Lewis S.E., Fichards S., Ashburner M.A., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Sabhurner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miltos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerya D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerya D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gerya D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Harlis N., Koldra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Sunders R.D.C., Scheeler F., Shen H.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.
"CDNA and amino acid sequences of Drosophila laminin B2 chain.";
Nucleic Acids Res. 16:7205-7205(1988).

-I- EUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

-I- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DUFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOU TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH ENDICATED SUBCELLULAR LOCATION: BASEMENT MEMBRANES (MAJOR COMPONENT).
                                                                                                                                                                                                                                                                                                 MEDLINE=88303364; PubMed=3405777;
                                                                                                                                                                                                                                                                                                                          STRAIN=OREGON-R;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Montell D.J., Goodman C.S.;
"Drosophila laminin: sequence of B2
three subunits during embryogenesis.
J. Cell Biol. 109:2441-2453(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90037237;
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                                                                                                                                                                                                                                                                               Hui C.-F
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dman C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10731132;
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EMBL; M58417; AAA28665.1; -.
EMBL; M25063; AAA28664.1; -.
EMBL; X07806; CAA30665.1; -.
EMBL; X07806; CAA30665.1; -.
PIR; A31483; MMFFB2.
HSSP; P02468; ITLE.
FlyBase; FBgn0002528; LanB2.
InterPro; IPR000561; EGF-like.
InterPro; IPR000186; LamMT.
InterPro; IPR000184; Laminin_B
InterPro; IPR000034; Laminin_B
InterPro; IPR002049; Laminin_EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SWOOD SMART; SMOOD SMART; SMOOD SMART; SMOOD SMART; SMOOD SMART; SMOOD SMOOD SMART; SMOOD SMART; SMOOD SMART; SMOOD SMART; SMOOD SMART; SMOOD SMART; PROSITE; PSO1186; EGF_2; 1.

PROSITE; PSO1248; LAMININ TYPE_EGF; 11.

PROSITE; PSO1248
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ProDom; PD003031; Laminin_B; 1.
SMART; SM00180; EGF_Lam; 10.
SMART; SM00001; EGF_11ke; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
SIMILARITY: CONTAINS 1 LAMININ -TERMINAL DOMAIN
SIMILARITY: CONTAINS 11 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pF00053;
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laminin_EGF; 10.
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LAMINI
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LAMININ N-TERMINAL (DOMAIN VI).
4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
Y SIMILARITY.
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IN EGF-LIKE 7.

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IN EGF-LIKE 10.

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IN EGF-LIKE 11.

D COIL (POTENTIAL).

D COIL (POTENTIAL).
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EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
DOMAIN IV.
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RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Davies P.,
RA Glodek A., Goong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Huuck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskarn D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,
Sylrak S.M., Wolson K.A., Walson M., Sung S., Yao Q.A.,
RA Wang Z.-Y., Washin M.P., Shin M., Yang S., Yao Q.A.,
RA Wall S., Ra, McMary S., Pan S., Pollard 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                              isolation of a collection of D. melanogaster cDNAs homologous to sequences in the Human Gene Index database.";
MO1. Gen. Genet. 261:64-70(1999).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 920 AND 930.
                                                                                                                                                                                                                                                              Caggese C., Ragone G., Perrini b.
Caizzi R., Barsanti P.,
"Identification of nuclear genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A60D_DROME (
P91927; Q9W160;
30-MAY-2000 (Re)
                                                                                                                                                                                                                                                                                                                MEDIINE-99168769; PubMed-10071211;
Caggese C., Ragone G., Perrini B., Moschetti R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D. Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 626-944 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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20-AUG-2001 (Rel. 40) Last and
CALCIUM BINDING MITOCHONDRIAL
ANON-60DA OR CG4589.
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          European
       Swiss Institute
Bioinformatics
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restrictions
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Baldwin D.,
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Q9USI6; P789
20-AUG-2001
20-AUG-2001
20-AUG-2001
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Pfam; PF00428; 60s_ribosomal; 1.

Pfam; PF01334; Bacteriofer; 1.

Pfam; PF02721; DUF223; 1.

Pfam; PF00036; efhand; 2.

Pfam; PF00036; HR1; 1.

Pfam; PF00056; Idh; 1.

Pfam; PF00056; RF1; 1.
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                                                                                                                                                                                                                                                                                                        29 ISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAIS
                                                                                                    LGLDNLTDDNAQRA-----ILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL
                                                                                        KDLSKLVNDIHDSAKEIQDIANEMRDKEETVPDKAKELKA-EPAFKDTAKTLKDNAKDL
                                                                                                                             LSDK------AIEELISLLDKEQVLQAE---QKIEKAIAKSMKEAEKLKSEVDKAD
                                                                                                                                           VLKETSDEA-RLKHIEAVLEKFDADKDGVVTVNDIRKVLES-----IGRDNIK
                                                                                                                                                                                                                                                                  DLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHAN 148
                                                                                                                                                                                     ASTNSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLE
                                                                                                                                                                                                         KD-GVISVNEITKAVQSIDREATNIDKKQLEEFTELLSKLASRRRHEEIVHIDDLMNNIK
                                                                                                                                                                                                                                                                                      VKEPVRESRAAKLLYNRVNKMISQLDNVL------NDLEARQHQIKQAESSDYAAS
                                                                                                                                                                                                                              KDKGAAELEKLFKAVENLSKAAQDTLKNAVKELT------SPIVHGNNSRKDGN 196
                                                                                                                                                                                                                                                 SPTVEPQQMVHIDELVATIRRMKEASDEERFKVVGD-----
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Y10912; CAA71853.1; A
                                 P78969
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                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s requires a license agreement (Some an email to license@isb-sib.ch).
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drion; Calci
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                                         STANDARD;
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 Last sequence up
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                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                            Score 156.5; Pred. No. 1.7; S2; Mismatches
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2) (IN REF. 2).

3 (IN REF. 2).

4 (IN REF. 2).

5 (IN REF. 2).

6 (IN REF. 2).

7 (IN REF. 2).

8 (IN REF. 2).
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update)
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                                                                                                                                                                                                                                                                                                                              141;
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Matches 88
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: REDUIRED FOR CELL DIVISION. IT IS A COMPONENT OF
CDC12 'SPOT', A STRUCTURE THOUGHT TO MARK THE SITE OF SEPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe.";
Cell Motil. Cytoskeleton 38:385-396(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYO2
                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                          Myosin; Actin-binding; ATP-binding; Coiled coil; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              May K.M., Watts F.Z., Jones N., Hyams J.S.;
Type II myosin involved in cytokinesis in the fission yeast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896
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SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAY WORK IN CONJUNCTION WITH MYO3.
                             QNENLQRESASLKQINNELESELLEKTS-----KVETLLSEQ-----NELKEKLSLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR SPCC645.
QCSTEFTNKLKS--EHAVLGLDNLTDDNAQ-RAILKKHANKDKGAAELEKLFKAVENLSK
                                                                                   KQQNSKSEVERDLVETNNSLTAVENLLTTERATALDKEETLRRTQERLANTEDSFSETKQ
                                                                                                               KDGNASANSADESVKGPN-LTEISKKITESNAVVLAVKEV----ETLLASIDE-----
                                                       ----LATKAIGKKIGNNGLEANOSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAK
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P08799; 1MND.
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                                                                                                                                          Score 154; DB Pred. No. 3.3; 76; Mismatches
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ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                 MYOSIN HEAD-LIKE
                                                                                                                                                                                                                D71D51D6578192BA CRC64;
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  (See http://www.isb-sib.ch/announce/
                                                                                                                                                       DB 1;
                                                                                                                                           139;
                                                                                                                                                                     Length 1526;
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                       PRINTS; PR00280; CHANLCOLICIN.

PRODOM; PD002657; Channel_colicin; 1.

PROSITE; PS00276; CHANNEL_COLICIN; 1.

Antibiotic; Bacteriocin; Plasmid; Transmembrane.

TRANSMEM 505 525 POTENTIAL.
                                                                                       EMBL; x87834; CAA61099.1; -.
EMBL; U27452; AAB41288.1; -.
InterPro; IPR000293; Channel_colicin.
Pfam; PF01024; Colicin; 1.
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          MEDLINE=96296448; PubMed=8709845;
Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
                                                                                           SEQUENCE FROM N.A. STRAIN=28691;
                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT)
                                                                                                                                                             Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                                                                                                                                   Borrelia burgdorferi (Lyme disease spirochete).
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EMBL; U04240; AAC45538.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 209 AA; 22393 MW; 3707/
                                                                                                                                                                                                                                                                                                                                    Q9S3P1;
                                                                                                                                                                                                                                                                                                                                                           Q9S3P1
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01-NOV-1996
01-NOV-1996
01-JUN-2001
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OSPC.
OSPC.
Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; SCBL_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stevenson B., Bockenstedt L.K., Barthold S.W., "Expression and gene sequence of outer surface burgdorfer reisolated from chronically infecters."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94314484; PubMed=8039931;
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Spirochaetaceae; Borrelia
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No. 4e-35;
          recombination
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Best Local S
Matches 184
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031117;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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                                                                                                                                                                                                                                                                        InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                           STRAIN-OC7;
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Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; SNCBI_TaxID=139;
                                                                                                                                                                                                                                                                 ProDom; PD001149;
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Mol. Microbiol. 18:257-269(1995).
EMBL; L42894; AAB37002.1;
                                                                                                                     1 MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA
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IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNK
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Similarity 100.0%;
84; Conservative
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192 AA;
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191 AA;
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Lipoprotein_6;
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EMBL/GenBank/DDBJ
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Last annotation updat
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                                                                                                                                                        Score 889; DB 2;
Pred. No. 1.3e-34;
2; Mismatches 2;
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01-JAN-1998 (TrEMBLrel. 05

01-JAN-1998 (TrEMBLrel. 05

01-JUN-2001 (TrEMBLrel. 17

f 01-JUN-2001 (TrEMBLrel. 17
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Wang I.-N. Dykhuizen D.E., Dunn J.J.,
Submitted (OCT-1997) to the EMBL/GenB.
Submitted (OCT-1997); AAB86554.1; -.
InterPro; IPRO01800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                          P94234 PRELIMINARY; PRT; 193 AA.
P94234; P194234; P194234; Ol-MAY-1997 (TrEMBLrel. 03, Created)
Ol-MAY-1997 (TrEMBLrel. 03, Last sequence update)
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
OSPC.
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BACTERIA (LA CONTROL DE LA CONT
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                        MEDLINE-96296448; PubMed-8709845;
Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
Lyme disease Borrella.";
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-28354;
                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme Bacteria; Spirochaetales;
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Best Local :
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Padula S.J., Sampieri A., Dias F., Szczepansk
Nolecular characterization and expression of
American strain of Borrelia burgdorferi.";
Infect. Immun. 61:5097-5105(1993).
EMBL; U01892; AAA16057.1; -.
InterPro; IPRO01800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD0011149; Lipoprotein_6; 1.
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Pred. No. 1.1e-23;
1; Mismatches 29;
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Pred. No. 4.3e-24;
0; Mismatches 25
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Q44720;
01-NOV-1996
01-NOV-1996
        SEQUENCE FROM N.A.
STRAIN-25015;
MEDLINE-95154673; PubMed-7851744;
Stevenson B., Barthold S.W.;
"Expression and sequence of outer surface particles of Borrelia burgdorferi."
FEMS Microbiol. Lett. 124:367-372(1994).
                                                                                                    Borrelia l
Bacteria;
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01-JUL-1997 (Tr
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01-SURFACE F
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SEQUENCE
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"B. tanukii(Strain Fi81t) ospC, partial cds.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ datal
EMBL; AB000354; BAA19087.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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NCBI_TaxID=56146;
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Hofmeister E.K., Glass G.E., Childs J.
"Population dynamics of a naturally oc
Borrella burgdorferi clones,";
Infect. Immun. 67:5709-5716(1999).
EMBL; AR074465; AAD23912.1; -.
InterPro; IPR001800; Lipoprotein_6.
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01-MAY-2000 (TYEMBLIEL. 13, Last sequence update)
01-JUN-2001 (TYEMBLIEL. 17, Last annotation updat
00TER SURFACE PROTEIN C PRECURSOR (FRAGMENT).
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 211 AA; 22603 MW; 63984BA6D8743ED5
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                    NKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAV 178
                                                                              KKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSV
                                                                                                                                                                         ISCNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKA
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201 AA;
                                                                                                                                                                                                                                                                 Conservative
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21457 MW;
                                                                                                                                                                                                                                                                                    35.8%; Score
73.4%; Pred.
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72.3%;
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Pred. No. 2.3e
l8; Mismatches
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                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                      644;
No. 2.
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1.7e-23;
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.3e-23;
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Best Local Sin
Matches 135;
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Q44726;
                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 17, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
BOTTCL1a burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID-139;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
0UTER SURFACE PROTEIN C (FRAGMENT).
MEDLINE=94314437; PubMed=8039891;
Fung B.P., McHugh G.L., Leong J.M., Steere A.C.;
"Humoral immune response to outer surface protein C of B
burgdorferi in Lyme disease: role of the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                                                SEQUENCE FROM N.A.
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EMBL; L42898; AAB37007.1; -
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193 AA;
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ilarity 72.6%;
Conservative 1
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                                                                                                                                                 Query Match
Best Local S
Matches 130
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Best Local S
Matches 136
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NON_TER
SEQUENCE
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MEDLINE-97478003; PubMed-9336916;
Ras N.M., Postic D., Foretz M., Baranton
"Borrelia burgdorferi sensu stricto, a ba
U.S.A.'?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TREMBLREL 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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EMBL; U08284; AAA21460.1; -
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        Marti-Ras N., Postic D., Foretz M., Baranton G.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases EMBL; U91798; AAB81895.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-TETS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                                   ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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192 AA;
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                                                                                                                                                 Score 623.5; DB Pred. No. 2.3e-22 Pred. No. 2.3e-22 Pred. Mismatches 3
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Pred. No. 4.4e-23;
0; Mismatches 26;
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Best Local Similarity
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                                        01-JAN-1998 (TremBLrel. 05, Created)
01-JAN-1998 (TremBLrel. 05, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
Bacteria;
  Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updato)
0UTER SURFACE PROTEIN C (FRAGMENT).
0SPC.
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel.
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InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99991544; PubMed=9872945; Wang I.N. Dykhuizen D.E., Qiu W., Dunn J.J., Bosler E.M., Luft B.J.; "Genetic diversity of ospc in a local population of Borrelia burgdorferi sensu stricto."; Genetics 151:15-30(1999).
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                                                                                                                                                                                                                                                                                         IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
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193 AA;
                                                                                                            PRELIMINARY;
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24; Mismatches 32;
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Best Local Similarity
Matches 129; Conserv
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SEQUENCE
                                                                                                                                                                                                                                                                                  Wang I.-N., Dykhuizen D.E., Dunn J.J., Luft B.J.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF029872; AAB86555.1; -. Interpro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1. ProDom; PD001149; Lipoprotein_6; 1.
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                                                    IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEFT 118
                                                                                                                                            ISCNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASVDELATKA 66
                                                                                                  IGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQELDGLKNSEKLKEKIENAKKCSEDFT
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185 AA;
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72.1%;
          2002, 10:10:55
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                                                                                                                                                                                                       Score 623; DB 2;
Pred. No. 2.3e-22;
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Result
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Perfect score:
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1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

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3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

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ALIGNMENTS

Chimeric - Borrelia Chimeric - Borrelia Borrelia sp chimeric ospC protein SEQ ID NO: 03-APR-2001 AAB62719; AAB62719 standard; Protein; 19-JUN-2000; 2000WO-US16915 28-DEC-2000 WO200078966-A1. Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick (first entry) ı sp. 367 B 42

Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease - $\,$

WPI; 2001-050113/06. N-PSDB; AAF29023.

Dattwyler RJ,

Seinost G,

Dykhuizen D,

Luft BJ,

Gomes-Solecki

(UYNY) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.

18-JUN-1999;

99US-0140042

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Best Local S
Matches 367
     Dattwyler RJ,
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Chimeric -
                                                    19-JUN-2000; 2000WO-US16915
                                         18-JUN-1999;
                                                                                  WO200078966-A1
                                                                                                                   Borrelia; ospC; Lyme
                                                                                                                             Borrelia sp chimeric ospC protein SEQ ID NO:
                                                                                                                                               03-APR-2001
                                                                                                                                                                         AAB62735 standard;
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                 UNIV NEW YORK STATE RES FOUND. BROOK BIOTECHNOLOGIES INC.
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67; Conservative
                                                                                               Borrelia
Borrelia
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    Seinost G,
                                       9908-0140042
                                                                                                                                                                         Protein;
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                                                                                                              disease; vaccine; chimeric protein; tick.
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     Dykhuizen
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Best Local Sim
Matches 366;
                                   19-JUN-2000; 2000WO-US16915
                                                                                                                                                              Chimeric - Borrelia
Chimeric - Borrelia
                                                                                                                                                                                                                                                            Borrelia sp chimeric ospC protein SEQ ID NO:
                                                                                                                           WO200078966-A1
                                                                                                                                                                                                                         Borrelia; ospC; Lyme disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions of OspC p
Lyme disease are used
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N-PSDB; AAF29039
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99.7%;
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Lyme disease are used
to Lyme disease -
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87.5%; Pred. No. 2.1e-93;
Live 20; Mismatches 25; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides from strains of Borrelia which cause to immunize animals and detect immune responses
                                                                                                                    disease;
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Borrelia
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Pred. No. 3
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Chimeric -
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DB; AAF29040.
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86.4%; Pred. No. 1.4e-91;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides compositions comprising ospc proteins and chimeric ospc proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 43; Page 81;
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2001-050113/06.
DB; AAF29015.
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                                                                                                                                                                                  The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                    Claim 43; Page 125-126; 160pp;
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       LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180
                         gkkihqnngldteynhngsllagayaistlikqkldglkneglkekidaakkcsetftnk
                                  GKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNK 120
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Borrelia sp.
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                                                                                                                                                                                                                                                                  s of Borrelia which cause detect immune responses
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                                                                     The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzeli or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
                                                                                                                                                          Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease -
                                                                                                                                                                                                                                                 (UYNY )
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                                                    Sequence
                                                                                                                                    Claim 43; Page 94-95; 160pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a \verb|sidelatkaig| k \verb|kiqqngg| lave a ghngtl lagay tisklitq k ldg lknsek lkekie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \verb|ltspvvaespamvnnsgkdgntsansadesvkgpnlteiskkitesnavvlavkeietl||
                                                                                                                                                                                                                                                  UNIV NEW YORK STATE RIBROOK BIOTECHNOLOGIES
                                                                                                                                                         disease
                                                                                                                                                                                                 AAF29020.
                                                                                                                                                                                                                                                                                                                                                                Borrelia
Borrelia
                                                    369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 chimeric ospC protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                99US-0140042
                                                                                                                                                                                                                               Seinost G,
                                                                                                                                                                                                                                                                                                                                                                                            Lyme disease;
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                                                                                                                                                                                                                              Dykhuizen
Score 1480; D. Pred. No. 2.2e 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO: 36
                                                                                                                                                                                                                                                                                                                                                                                            chimeric protein; tick.
 DB 22;
2.2e-88;
nes 31;
                                                                                                                                                                                                                               Luft
                                                                                                                                                                                                                               ВJ,
                      Length
                                                                                                                                                                                                                                Gomes-Solecki
                       369;
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                      The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads
                                                                   Claim
                                                                                    Compositions of OspC polypeptides from strains of Borrelia which Lyme disease are used to immunize animals and detect immune responded to Lyme disease.
                                                                                                                                                                                                          19-JUN-2000;
                                                                                                                                                                                                                                           WO200078966-A1.
                                                                                                                                                                                                                                                            Chimeric - Chimeric -
                                                                                                                                                                                                                                                                                      Borrelia;
                                                                                                                                                                                                                                                                                                       Borrelia
                                                                                                                                                                                                                                                                                                                        03-APR-2001
                                                                                                                                                                                                                                                                                                                                         AAB62739;
                                                                                                                                                                                                                                                                                                                                                          AAB62739 standard; Protein; 400
Sequence
                                                                                                                                               Dattwyler RJ,
                                                                                                                                                                                                                           28-DEC-2000
                                                                                                                                                                (BROO-)
                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE RES FOUND
                                                                                                                                                                                         18-JUN-1999;
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                Lyme
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)B; AAF29043.
                                                                                                                                                                                                                                                                                                                                                                                                    emlansvkel 369
                                                                                                                                                                                                                                                                                                                                                                                                                     EMLANSVKEL 368
                                                                   43;
                                                                                                                                                                BROOK BIOTECHNOLOGIES
                disease.
                                                                                                                                                                                                                                                                                                      qs
                                                                  Page 153;
                                                                                                                                                                                                                                                                                      ospC; Lyme disease;
                                                                                                                                                                                                                                                            Borrelia
Borrelia
400
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Query Match

82

38

Score 1479.

. 5;

DВ

22;

Length 400

The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelid or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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                                                                                                                                                  Compositions of OspC |
Lyme disease are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
Chimeric -
                                                                                          Claim 43; Page 131; 160pp;
                                                                                                                                                                                                           N-PSDB; AAF29035
                                                                                                                                                                                                                                                                  Dattwyler RJ,
                                                                                                                                                                                                                                                                                                                                                               18-JUN-1999;
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                                                                                                                                  disease
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Borrelia
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                                                                                                                                                                                                                                                                                                         BIOTECHNOLOGIES INC.
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                                                                                                                                                   polypeptides from strains of Borrelia which cause d to immunize animals and detect immune responses
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                                                                                            English.
                                                                                                                                                                                                                                                                    Dykhuizen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393
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    Compositions of OspC polypeptides Lyme disease are used to immunize to Lyme disease -
                                    WPI; 2001-050113/06
N-PSDB; AAF29016.
                                                                                                                                        WO200078966-A1
                                                                                                                                                       Chimeric - Chimeric -
                                                                                                                                                                            Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick
                                                                                                                                                                                          Borrelia sp chimeric ospC protein SEQ ID NO:
                                                                                                                                                                                                          03-APR-2001 (first entry)
                                                                                                                                                                                                                                     AAB62712 standard; Protein; 378 AA
                                                         Dattwyler RJ,
                                                                                             18-JUN-1999;
                                                                                                           19-JUN-2000; 2000WO-US16915.
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                                                                                                                                                                                                                                                                                   EMLANSVKEL 368
                                                                                                                                                                                                                                                                                                                                   KELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASI 238
                                                                                                                                                                                                                                                                                                                                                                                                                            GKKIGNNG-LEANQSKNTSLLSGAYAISDLIAEKLNVLKNEE-LKEKIDTAKQCSTEFTN 119
                                                                                                                                                                                                                                                                             emlansvkel
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                                                                      UNIV NEW YORK STATE RES FOUND BROOK BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                       Borrelia
Borrelia
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                                                        Seinost G,
                                                                                             99US-0140042
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                                                                                                                                                       gp.
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                                                        Dykhuizen D,
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
           from strains animals and o
                                                        Luft BJ,
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            s of Borrelia which cause detect immune responses
                                                        Gomes-Solecki
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Chimeric -
                   Dattwyler RJ,
                                                                         18-JUN-1999;
                                      (UYNY ) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                                            19-JUN-2000; 2000WO-US16915
                                                                                                                                       WO200078966-A1
                                                                                                                                                                                             Borrelia; ospC; Lyme disease;
                                                                                                                                                                                                                 Borrelia sp
                                                                                                                                                                                                                                       03-APR-2001
                                                                                                                                                                                                                                                               AAB62710;
                                                                                                                                                                                                                                                                                 AAB62710 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides compositions comprising ospC proteins an chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads to Lyme disease.
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70.3%;
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                                                                                                                                                                                          vaccine; chimeric protein; tick.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses
                                                                              Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                         Borrelia sp chimeric ospC
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                          19-JUN-2000;
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        18-JUN-1999;
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                          2000WO-US16915
                                                                                                                                            (first entry)
        99US-0140042
                                                                                                       Lyme disease;
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2.1e-73;
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Lyme disease are used
to Lyme disease -
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                                                                                                                                                                                                                                                                                                                                              Claim 43;
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N-PSDB; AAF29032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNY ) UNIV NEW YORK STÄTE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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                    kakkcseeftaklkgehtdlgkegvtddnakkailktnndktkgadeleklfesvknlsk
                             NAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAK
                                                     ASIDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIE
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                                                                                                                                                                                                                                                                                            disease.
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164.485 Million cell updates/sec
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                                                                                                                                                                 Description
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ALIGNMENTS

US-09-596-746A-42

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; FEATURE:
; OTHER INFORMATION: OSPC Chimera
US-09-596-746A-42
                                                                                                                                                                                 SOFTWARE: Fa
SEQ ID NO 42
LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42, Application US/09596746A GENERAL INFORMATION:
Matches 368;
             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Groups of Borrelia burgdorferi
TITLE OF INVENTION: Borrelia afzelii That Cause Lyn
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                      FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Dattwyler, Raymond J.
Seinost, Gerald
 Conservative
                 100.0%;
0;
Score 1798; DB 19;
Pred. No. 5.6e-124;
); Mismatches 0;
 Indels
                                Length 368;
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; OTHER INFORMATION: OSPC Chimera
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SEQ ID NO 42
LENGTH: 367
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                     Query Match
Best Local Similarity
Matches 367; Conserv
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                            KSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKEL 181
TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDEL
                                                                   GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL
                                                                             GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL 121
                                                                                                          SEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEM
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                                                                                                                                                  Score 1793; DB 19;
; Pred. No. 1.3e-123;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          Cause Lyme Disease in Humans
                                                                                                                                                                     Length 367;
                                                                                                                                                   Indels
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APPLICANT: Scinost, Gerald
APPLICANT: Scinost, Gerald
APPLICANT: Scinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Groups of Borrelia burgde
TITLE OF INVENTION: Groups 
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; ORGANISM: OSPC
US-09-596-746-74
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SOFTWARE: Fas
SEQ ID NO 74
TRNGTH: 391
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; GENERAL INFORMATION:
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Best Local
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                             ANSVKEL 368
                                                                                     ATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCS
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  ANSVKEL
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Pred. No. 2.4e-123;
1; Mismatches 0;
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hat Cause Lyme Disease
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Sequence 40, Application US/09596746A

GENERAL INFORMATION:
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SEQ ID NO 74
LENGTH: 392
TYPE: PRT
ORGANISM: OSPC Chimera
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Best Local S
Matches 366
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APPLICANT: MARIA J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
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APPLICANT: Dattwy.e.,
APPLICANT: Seinost, Geraid
APPLICANT: Seinost, Geraid
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdc
TITLE OF INVENTION: Borrelia afzeili That Car
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 40
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                      US-09-596-746-40
                                                                                           CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                      Sequence 40, Applica GENERAL INFORMATION:
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Best Local Similarity
OTHER INFORMATION: OSPC Chimera -09-596-746-40
                               LENGTH: 368
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                              FastSEQ for Windows Version 4.0
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Pred. No. 1.3e-106;
20; Mismatches 25; J
                                                                                                                                                                                                                       Borrelia burgdorferi and afzelii That Cause Lyme D
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87.5%;

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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia fizelii That Cause Lyme Dises
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 392
TUPEN: DDM
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                                                                                                                                                                                                                      ; ORGANISM: ospC Chimera US-09-596-746-72
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US-09-596-746-72
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Best Local Similarity
Matches 320; Conser
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APPLICANT: Dattwyler, Raymond J.
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APPLICANT:
APPLICANT:
APPLICANT:
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Matches
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nes 321; Conservative
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                                                         GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL 144
                                                                          GKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKL 121
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Luft, Benjamin J.
Maria J.C. Gomes-Solecki
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                                                                                                                                                           Conservative
                                                                                                                                                                     86.5%;
                                                                                                                                                          21;
                                                                                                                                                      Score 1554.5; DB 19; Length 392;
Pred. No. 5.4e-106;
21; Mismatches 25; Indels 1;
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0; Mismatches 25;
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US-09-596-746A-72
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SEQ ID NO 72
LENGTH: 393
TYPE: PRT
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 385 TNSVKEL
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                      ANSVKEL 368
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391
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GENERAL INFORMATION:

APPLICANT: Dattwyler, Raymond J.

APPLICANT: Seinost, Gerald

APPLICANT: Seinost, Gerald

APPLICANT: Dykhulzen, Danial

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki

TITLE OF INVENTION: Groups of Borrelia burgdorferi and

TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in I

FILE REFERNCE: 2631.1002-001

CURRENT APPLICATION NUMBER: US/09/596,746A

CURRENT APPLICATION NUMBER: US/09/596,746A

CURRENT FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84

SOFTWARRE: FASTERO for Windows Version A 0
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Best Local Similarity
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                                                                                    A-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAEIEKAKKCS
                                                                                                                                                                                              TSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDEL
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                          EDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEML 361
                                                                                                        ATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCS
EEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEML
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87.2%;
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Pred. No. 5.56
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; OTHER INFORMATION: OspC Chimera
US-09-596-746-38
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SOFTWARE: FRSELSEQ for
SEQ ID NO 38
LENGTH: 368
TYPE: PRT
Sequence 3B, Application US/09596746A

GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
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Best Local Similarity 86.7
Matches 319; Conservative
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Luft, Benjamin J.
Maria J.C. Gomes-Solecki
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 1000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1990-06-18
                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-596-746-76
Sequence 76, Application US/09596746
GENERAL INFORMATION:
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; ORGANISM: ospC Chimera
US-09-596-746-76
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CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 76
LENGTH: 391
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TYPE: PRT
ORGANISM: Artificial Sequence
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                               TYPE: PRT
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86.7%;
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Pred. No. 8.1e-105;
Prematches 27;
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Best Local Similarity
Matches 317; Conserv
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Best Local S
Matches 317
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APPLICANT:
                                                                                                                                                                                                              LENGTH: 392
TYPE: PRT
ORGANISM: OSPC Chimera
-09-596-746A-76
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nes 317; Conserv
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KSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLEKAVENLSKAAQDTLKNAVKEL 181
                                                                                         SCNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAI 85
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Maria J.C. Gomes-Solecki
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                                                                                                                                             85.1%; score 1530; DB 19;
86.4%; Pred. No. 3.5e-104;
htive 21; Mismatches 27;
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86.4%; Pred. No. 3.5e-104;
71. Mismatches 27;
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SEQ ID NO 26
LENGTH: 374
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Best Local Similarity 83.4%; Pred. No. 3.4e
Matches 312; Conservative 22; Mismatches
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TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR PILICATION NUMBER: US 60/140,042
NUMBER OF SEQ ID NOS: 84
SOPTMARES SECTION 
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FastSEQ for Windows Version 4.0
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Seinost, Gerald
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APPLICANT: Dattwyler, Raymond J.

APPLICANT: Scinost, Gerald

APPLICANT: Scinost, Gerald

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki

TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea

TILE REFERENCE: 2631.1002-001

CURRENT APPLICATION NUMBER: US/09/596,746

CURRENT PILING DATE: 2000-06-16

CURRENT PILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 84

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 377

TYPE: PRT

ORGANISM: Artificial Sequence
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                                                                       RESULT 15
US-09-596-746A-30
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            Sequence 30, Application US/09596746A
GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
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Dykhuizen, Danial
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23; Mismatches
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es 34; Indels 9;
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER: OF SEO ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 30
LENGTH: 377
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Best Local :
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Local Similarity 82.5%; Pred. No. 6.26
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Maria J.C. Gomes-Solecki
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000000000
    US-08-235-836C-122
US-08-235-836C-110
US-08-158-353-3
US-08-158-353-3
US-08-158-353-3
US-08-235-836C-30
US-08-235-836C-30
US-08-235-836C-30
US-08-235-836C-34
US-08-335-836C-34
US-08-35-836C-34
US-08-35-836C-34
US-08-35-836C-34
US-08-35-836C-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (without alignments)
149.211 Million cell updates/sec
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Sequence 122, App
Sequence 107, App
Sequence 110, App
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 32, Appli
Sequence 33, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
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                                                                                                REFERENCE/DOCKET NUMBER: BNL9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
TELEPHONE: (516) 282-7329
INFORMATION FOR SEO ID NO: 122:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-836C-122
    Ş
                             Query Match 38.9%; Score 699; DB 4; I Best Local Similarity 41.5%; Pred. No. 5.1e-45; Matches 195; Conservative 49; Mismatches 104;
    7 GKDGNASANSADESVKG------PNLTEISKKITESNAVVLAVKEVET----LLASID 54
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Result

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BNL93-28A

Length 588; Indels 122;

Gaps

17;

US-08-235-836C-122 Sequence 112, Application US/08235836C Patent No. 6248562 GENERAL INFORMATION: APPLICANT: Luft, Benjamin J. APPLICANT: Luft, Benjamin J. TITLE OF INVENTION: No. 6248562el Chimeric TITLE OF INVENTION: No. 6248562el Chimeric TITLE OF INVENTION: No. 6248562el Chimeric TITLE OF INVENTION: Norrelia Polypeptides a NUMBER OF SEQUENCES: 144 CCRRESPONDENCE ADDRESS: ADDRESSEE: Brookhaven National Laboratory STREET: CITY: Upton STATE: NY COUNTRY: USA ZIP: 11973 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-TOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION NUMBER: US 08/08/235,836C FILING DATE: 29-APR-1994 CLASSIFICATION INDATA: APPLICATION NUMBER: US 08/148,191 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION: NAME: BOGOSIAN, MATGGGGGG REGISTRATION NUMBER: 25,324 REGISTRATION NUMBER: 25,324 REGISTRATION NUMBER: 25,324	28 146.5 8.1 1164 4 US-08-923-992A-2 29 146.5 8.1 1786 4 US-08-973-462-8 30 145 8.1 1147 3 US-08-470-260-5 31 145 8.1 1147 3 US-08-477-491-5 32 145 8.1 1147 3 US-08-477-451-2 33 145 8.1 3289 2 US-08-466-662-5 34 142 7.9 688 3 US-09-141-047-8 35 141.5 7.9 3111 2 US-08-466-309-4 36 141.5 7.9 3111 2 US-08-466-390-4 37 141 7.8 2101 1 US-08-466-390-4 38 141 7.8 2101 1 US-08-47951-4 40 141 7.8 2101 1 US-08-47951-4 41 141 7.8 2101 1 US-08-47981-4 42 141 7.8 2101 1 US-08-47981-4 43 141 7.8 2101 2 US-08-483-924-4 44 138.5 7.7 1128 4 US-08-933-924-6 45 136.5 7.6 679 4 US-08-913-942-15	
ic Proteins Comprising s and Uses Therefor ory.	Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 15, Appli Sequence 15, Appli	

Length Indels

37;

Gaps

8

324

383

443

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US-08-235-836C-107; Sequence 107; Application Patent No. 6248562; GENERAL INFORMATION:
                                                                                    TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-11-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 282-7338
TELEFAX: (516) 282-3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 GVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 NYTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/235,836C FILING DATE: 29-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                         NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 11973
TOPOLOGY:
                    TYPE:
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSADESYKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSADESYKGPNLTEISKKITESNAVYLAYKEIETLLASIDELATKAIGKKIQQNGGLAV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVELKGTSDK--NNGSGTLEGSKPDKSKVKLTVSADLNTVTLEAFDA-SNQKISSKV-TK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYNHNGSLLAGRYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFTNKLKEKHTDLGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTDGTITVQQYNTAGTSLEGSASEIKNLSE-----LKNALK--GHPM--GNNSGKDGNTS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSQKENDLNLEDSSKKSHQNAKQDLPAVTEDSVSLFNGNKIFVSKEKNSSGKYDLRATID 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTVEIKEGTVTLKREIEKDGKVKVFLNDTAGSNKKTGKWEDSTSTLTISADSKKTKDLVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------KGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIVHGNNSGKDGNTS 198
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                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6248562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.8%; Score 698.5; DB 4; Best Local Similarity 47.7%; Pred. No. 4.1e-45; Matches 177; Conservative 43; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 110, Application US/08235836C
                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                   REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin
TITLE OF INVENTION: No. 62
TITLE OF INVENTION: Boxrel
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 KEMLANSVKEL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 LK-----MANNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSS
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Upton
STATE: NY
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                      TELEPHONE:
                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSLLSGAYAISDLIAEKLNVLKNE---ELKEKIDTAKQCSTEFTNKLKSEHAVLGLDNLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEMLANSVKEL 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVFKEDGKTLVSKKVTSKDKSSTEEKFNEKGEVS-EKIITRADGTRLEYTGIKSDGSGKA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDETAAKAIGKKIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKN-EGLKEKIDAA
                                                                                                      Bogosian, Margaret C
                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
: (516)
(516) 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           njamin J.
No. 6248562el Chimeric Proteins Comprising
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                                                                   BNL93-28A
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US-08-158-353-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08158353 Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 466 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Padula
                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAITOIL, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: UCT9
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEPAX: 617-861-9540
TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309
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                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                          ZIP: 02173
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                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SK-DKSSTEEKFNEKGE----VSEKIITRADGTRLEYTGIKSDGSGKAKEVL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQ-LGIENVTDENAKKAI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELTSPIVHGNNSGKDGNTSA----NSADESVKGPNLTEISKKITESNAVVLAVKEIETLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEETN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATVDKLELKGTSDKNNGSGVLEGVKADKSKVKLTISDDLGQTTLEVFKEDGKTLVSKKVT
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                                                                                                                                                                                                                                                                                                                                                                                               Hamilton, Brook,
                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven J.
Methods for Diagnosing Early Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disease
                                                                                                                                                                                      US/08/158,353
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-158-353-2
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                                                             В
                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-09-196-293-15
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NO...
SOFTWARE: FastSEQ for W
SEQ ID NO 15
FENGTH: 209
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                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1998-11-19

EARLIER APPLICATION NUMBER: US 08/209,603

EARLIER FILING DATE: 1994-03-10

EARLIER APPLICATION NUMBER: US 07/862,535

EARLIER FILING DATE: 1992-06-19

EARLIER APPLICATION NUMBER: WO PCT/EP90/02282

EARLIER FILING DATE: 1990-12-21

EARLIER APPLICATION NUMBER: DE P39 42 728.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Active proteins from Borrelia TITLE OF INVENTION: burgdorferi FILE REFERENCE: 738.001US2
                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1989-12-22
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fuchs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT
                                                             120 KLKSEHAVLGLDN--LTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
                              249
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               KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/196,293
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                                                                                                                                Conservative
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                                                                                                                           35.8%; Score 644.5; DB 4; 75.6%; Pred. No. 1.6e-41; rs. Mismatches 28;
                                                                                                                                                                                                                                                                                               Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.6%;
72.9%;
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Pred. No. 1.7e-42;
                                                                                                                                                              Length 209;
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US-08-235-836C-30

Sequence 30, Application US/08235836C

Patent No. 6248562

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
APPLICANT: Dunn, John J.

APPLICANT: Luft, Benjamin J.

APPLICANT: Luft, Benjamin J.

TNYENTION: No. 6248562el Chimeric Proteins Comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for Diagnosing Early Lyme
TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                     309 EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02173
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                                                                                                                                                                                                                                                                      KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFTNKL
                                                                                                                                                                                                     KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                         35.8%;
75.6%;
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; Pred. No. 1.6e-41
15; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FUCHS, RENATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNLS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFTWARE: PATE:....
SOFTWARE: PATE:.....
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
APPLICATION APPR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                           APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTIN
APPLICANT: PREAC-MURSIC,
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ER
                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                        TITLE OF INVENTION: IMMUNOLOGICALITITLE OF INVENTION: FROM BORRELIA NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-APR-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                      309 EGEHAQLGIENVIDENAKKAILIIDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248
                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFTNKL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USE FILING DATE: 01-11-93
                                    CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Brookhaven National Laboratory
COUNTRY:
                  STATE:
                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
                                                                                                                                                                                                                                                                                                                                                                                     KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135;
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                 NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: 210 amino acids amino acid
                                                     99 PARK AVENUE
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USA
                                                                                                                                                                                             WILSKE, BETTINA
PREAC-MURSIC, VERA
                                                                                                                                                             SOUTSCHECK, ERWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                    BROOKS HAIDT HAFFNER & DELAHUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (516) 282-7338
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75.0%;
                                                                                                                                              IMMUNOLOGICALLY ACTIVE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 639.5; DB 4;
Pred. No. 3.9e-41;
Pred. No. 3.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BNL93-28A
                                                                                                                           BURGDORFERI
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Sequence 2, Application US/08031295
Patent No. 5530103
GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IDENTIFICATION METHOD: ; PUBLICATION INFORMATION: US-08-209-603E-15
                                                                                                                                                                                                            RESULT 9
US-08-031-295-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: N/A
ANTI-SENSE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/EP90
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/86
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: B. BURGD
IMMEDIATE SOURCE:
LIBRARY: DSM 5662
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSOR PROPERT TYPE: N/A
PRIGINAL SOURCE:
ORIGINAL SOURCE:
B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: AT&T - IBM COOPERATING SYSTEM: MS-DOSOFTWARE: ASCII CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10016
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                    309 EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL 368
                                                                                                                                                                                                                                                                                     139
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                                                                                                                                                                                                                                                                                                                                                         90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 10-MAF
                                                                                                                                                                                                                                                                                                                                                                                                                            20 NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVLEVEALLSSIDEIAAKAIGK 79
                                                                                                                                                                                                                                                                                                                                                       KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIDAAKKCSETFTNKL 138
                                                                                                                                                                                                                                                                                                                                                                          KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
                                                                                                                                                                                                                                                                                 KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: 3.5" FLOPPY DISC
ER: AT&T - IBM COMPATIBLE
ING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSM 5662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N/A
                                                                                METHOD AND COMPOSITION FOR THE PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.5%; Score 637.5; DB 4; 75.0%; Pred. No. 5.5e-41; tive 15; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/209,603E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid analysis N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210;
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US-08-031-295-2
                                                                                                                                                                                                                               US-07-903-580-2
                                                                                                                                                                                      Sequence 2, Application US/07903580 Patent No. 6221363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 127; Conserv
                                                  APPLICANT: LIVEY, IAN
APPLICANT: DORNER, Freidrich
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND
TITLE OF INVENTION: PREVENTION
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    200 L 200
                                                                                                                                                                                                                                                                                                                                    368 L 368
                            STREET:
                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                          3: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                               METHOD AND COMPOSITION FOR PREVENTION OF LYME DISEASE
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/1

FILING DATE: 22-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/2

FILING DATE: 11-TUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,761
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
APPLICATION STEEL 25-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 2000/-5103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
140 LAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANSVKE
                                                                                                          248 KKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKK 307
                                                                                                                                                                                                 189 NNSGKDGNT-SANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIG 247
                         308 LEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                    80 KKIQQNNGLGANADKNGSTLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDETKK 139
                                                                                                                                                                              20 NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATKAIG
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FILING DATE: 19930312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202)672-5300
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                   33.4%; Score 600.5; DB 1; 70.2%; Pred. No. 3.4e-38; tive 20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/727,245
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                                                                                                                                                                                                                                                                                                               Length 212;
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COUNTRY:

Virginia

22313-0299

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RESULT 11
US-08-158-353-4
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                                                                                                                                                                          Sequence 4, Application US/08158353
Patent No. 5620862
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                            STREET: IWC
CITY: Lexington
CTATE: MA
TRANTE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: 19920625
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  200 L 200
                                                                                                                                                                                                                                                                                                                368 L 368
                                                                                                                                                                                                                                                                                                                                      140 LAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANSVKE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                     308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                 COUNTRY: U
ZIP: 02173
                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 212 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0:
FILING DATE: 22-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                LEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKE 367
                                                                    E: Hamilton, Brook, Two Militia Drive
                                                                                                                         Padula, Steven J.
VENTION: Methods for Diagnosing Early Lyme
VENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.4%; Score 600.5; DB 4; Length 212; 70.2%; Pred. No. 3.4e-38; tive 20; Mismatches 33; Indels 1
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                                                                                 Smith & Reynolds,
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US-08-235-836C-34
; Sequence 34, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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Best Local Similarity
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin J.
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
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                                                                                                                                                                                                                                 STREET:
CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 VKELTSPVV 205
                                                                                                                                                                                COUNTRY: USA
ZIP: 11973
                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                   ADDRESSEE: Brookhaven National Laboratory
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
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68.8%; Pred. No. 2.70
tive 20; Mismatches
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APPLICATION NUMBER: US 0 FILING DATE: 01-11-93 ATTORNEY/AGENT INFORMATION:

US 08/148,191

BNL93-28A

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APPLICANT: SOLUSIONES, ETWIN
APPLICANT: Wilske, Bettina
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorfer1
FILE REFERENCE: 738.001US2
CURRENT APPLICATION UNUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
CEARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: DE 728.5
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1989-12-22
EARLIER FILING DATE: 1989-12-22
EARLIER FILING DATE: 1989-12-22
EARLIER FILING DATE: 1990-06-13
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; ORGANISM: Borrelia burgdorferi
US-09-196-293-11
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Best Local Similarity
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                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Patent No. 618375
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INFORMATION FOR SEQ ID NO:
                                                                                                                                 NUMBER OF SEQ ID NOS:
                                           TYPE: PRT
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LENGTH: 212 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNI
TELECOMMUNICATION INFORMATION:
TELECHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197
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                                                                                                              Windows Version 4.0
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Patent No. 6
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Best Local Similarity
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                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                         TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T' - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOTZ, MANERED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTITLE OF INVENTION: FROM BORRELIA BURGDORFERI
NUMBER OF SEQUENCES: 15
              HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WILSKE, APPLICANT: PREAC-M
FRAGMENT TYPE:
                                                                      MOLECULE TYPE:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 99 PARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994
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                                              DESCRIPTION:
                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 AIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEF 136
                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKN-EELKEKIDTAKQCSTEF 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILSKE, BETTINA
PREAC-MURSIC, VERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
         N/A
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                                                                                   LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BROOKS HAIDT HAFFNER & DELAHUNTY
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ORGANISM:

B. BURGDORFERI

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APPLICATION NUMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGATEC:
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BUJ3-28A
TELEPHONE: (516) 282-738
TELEPHONE: (516) 282-739
INFORMATION STARRAGENTION: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-235-836C-36
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; ORIGINAL SOURCE:
US-08-209-603E-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36, Application US/08235836C Patent No. 6248562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.2
Best Local Similarity 68.3
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
Lational Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: PUBLICATION INFORMATION: ANTI-SENSE: N/A
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POSITION IN GENOME: N/A
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STATE: NY
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17 ISCNNSGKVGILTSTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKK 76
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Best Local Similarity 62.6%;
Matches 117; Conservative
                                                 134 KLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAALTNSVK 193
                                                              120 KLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVK 179
194 ELTNPVV 200
                         180 ELTSPIV 186
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                                                                                                                       IGKKIGNNG-LEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTN 119
                                                                                                                                                                                                                                                                                                                                       amino acid
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Search completed: March 18, 2002, 09:55:35 Job time: 348 sec

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GenCore version Copyright (c) 1993 - 2000

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ALIGNMENTS

outer surface protein C precursor - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000 C;Accession: I40142; S70283 R;Stevenson, B.; Bockenstedt, L.K.; Barthold, S.W. Infect. Immun. 62, 3568-3571, 1994 A;Cross-references: EMBL:U04240; NID:g2314877; PIDN:AAC45538.1; PID:g434658 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448 RESULT I40142 A;Gene: ospC C;Superfamily: Lyme disease spirochete surface protein A; Reference number: A; Accession: S70283 A;Title: Expression and gene sequence of outer surface A;Reference number: I40142; MUID:94314484 A;Accession: I40142 A;Status: nucleic acid sequence not shown A; Residues: 1-209 < RES> A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA Matches 184; Query Match Best Local Similarity 17 ISCNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA 76 1 MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA 60 ::|||||||||||||||||| Conservative 50.1%; 2 Score 901; DB 2; Pred. No. 4.4e-36; 2; Mismatches 0 0; Length 209 Indels protein C 0 of Borrelia burgdorf Gaps 'n 0;

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LTSPIV

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181 LTSPIV 186

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LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180

LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE

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C;Superfamily: Lyme disease spirochete surface protein
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Cession: 140153
A: Molecule type: DNA
A: Residues: 1-191 < RES>
A: Cross-references: EMBL:U08284; NID:g469561; PIDN:AAA21460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            outer surface protein C - Lyme disease spirochete (fragment) C:Species: Borrelia burgdorferi (Lyme disease spirochete) C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C:Accession: I40153
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outer surface protein C - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
C;Accession: S70287
R;Livey, I; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in OspC variation A;Reference number: S70255; MUID:96296448
A;Accession: S70287
A;Accession: S70287
                                                                                                                                                                                                                                                                                                                                                     Infect. Immun. 62, 3213-3221, 1994
A;Title: Humoral immune response to outer surface protein
A=Beference number: 140153; MUID:94314437
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Best Local Similarity
Matches 178; Conserv
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                                                         KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL
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Pred. No. 2.4e-34;
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6e-35;
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                                                                                                                                                                                                       Length 191;
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A; Gene: ospC
C; Superfamily:
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R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Leb
J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrella burgdorferi outer surface
A;Reference number: 140104; MUID:95286481
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X84785; NID:g793787; PIDN:CAA59256.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-178 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outer surface protein C - Lyme disease spirochete (strain 272) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000 C;Accession: I40104; S54184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDB.
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A:Title: Evolution of the Borrelia burgdorferi outer surfa
A:Reference number: I40104; MUID:95286481
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A; Residues: 1-178 < RES>
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A; Accession: I40125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local :
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Best Local
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GIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLPKAAKEMLANSVKEL
                     GIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
                                                                                                  LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKLEGEHAQL
                                                                              LAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLTEKIENAKRCSEDFTKKLEGEHAQL
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Pred. No. 1.7e~32;
1; Mismatches 2;
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Pred. No. 1.2e-32;
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A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RES>
A;Cross-references: EMBL:X84782; NID:g793815; PIDN:CAA59253.1; PID:g793816
C;Superfamily: Lyme disease spirochete surface protein C
                                            В
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A;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of Borrel. A;Reference number: I40047; MUID:95395018
A;Accession: S69927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Borrelia burgdorferi (Lyme disease spiro A; Variety: strain PKa C;Date: 15-Feb-1997 #sequence_revision 27-Feb-1997 C;Accession: S69927; S72669
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A;Residues: 1-124,'D',126-139,'E',141-210
A;Cross-references: EMBL:X69589
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A; Accession: S72669
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R;Thelsen, M.; Borre, M.; Mathlesen, M.J.; Mikkelsen,
J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer
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                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library,
                                                                                                                                  Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                               Genetics:
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249 KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL
                                                                                    189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248
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                                                                                                                                     Local Similarity
les 137; Conserv
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                                                                                                                                     14;
                                                                                                                                Score 648.5; DB 2;
Pred. No. 3.2e-24;
4; Mismatches 28;
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Pred. No. 1.5e-28;
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Outer surface protein C precursor - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C;Accession: I40145
R;Fukunaga, M.; Hamase, A.
J. Clin. Microbiol. 33, 2415-2420, 1995
A;Title: Outer surface protein C gene sequence
A;Reference number: I40269; MUID:96025162
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C;Superfamily: Lyme disease spirochete surface
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FEMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer
A;Reference number: I40143; MUID:95154673
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                                                                                                                                                Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease
A; Reference number: A70100; MUID:98065943
A; Accession: G70218
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                                                                  A; Molecule type: DNA
A; Residues: 1-211 <RES>
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                                                                                                 A; Molecule type: DNA
A; Residues: 1-210 <KLE>
                                                                                                                                    A;Status: nucleic acid sequence not shown; translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MACNNSGKDGN-ASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKLKSSHTELGKQDAQDDDAKKAILRTHNTKDKGAEELDKLFKAVENLSKAAKEMLSNSV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTIDUCKEGVIDADAKEAILKINGIKIKGAEELGKLFESVEVLSKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKN-EGLKEKIEAAKKCSETETNKL
                                                                                                                                                                                                                                                                                                                                                                                                                            KELTSPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELTSPIV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGKKIHQNNGLDTENNHNGSLLAGAYAISTLITQKLGGLKNEELKEKIAAVKKCSEEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIGKKI-GNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL:U04282; NID:g2314881; PIDN:AAC45540.1; PID:g434666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.9%;
72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                   NID:g3253098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 646; DB 2;
Pred. No. 4.2e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surface protein
                                                                                                                                                                                    spirochaete,
                   analysis
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                                                                                     PIDN: AAC66329.1;
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                                                                                                                                     not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                   of
                                                                                                                                                                                      Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C
                   Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               among
                                                                                   PID:g2689901;
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                   burgdorferi
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                                                                                     TIGR: BB
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A:Residues: 1-193 <LIV>
A:Cross-references: EMBL:L42898; NID:9858729;
A:Experimental source: strain 25015
                                                                                                                                                                                                                                                                                                    R;Livey, I.; Glbbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination in A;Reference number: S70255; MUID:96296448
A;Accession: S70279
                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown
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A;Title: Evidence for lateral transfer and recombination in OspC variation in A;Reference number: S70255; MUID:96296448
A-Accession: S70281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross*references: GB:049497; NID:9707092; PIDN:BAA08457.1; PID:9769684
R;Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Med. Microbiol. Immunol. 182, 37-50, 1993
A;Title: Genetic heterogenity of the genes coding for the outer surface I A;Reference number: S37726; MUID:93268136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: ospC
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain Ip2 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-210 <JAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: DNA A:Residues: 1-210 <RES>
                                                                                                                                                               ;Superfamily: Lyme disease spirochete surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                       Matches 135;
                                                                                                         Query Match
Best Local :
                                                                                                                                                                                         Gene:
                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                   r surface protein C - Lyme disease spirochete ecles: Borrella burgdorferi (Lyme disease spirochete) Date: 12-reb-1998 #sequence_revision 20-reb-1998 #text_change Accession: S70279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actus: nucleic acid sequence not shown blecule type: DNA Residues: 19-210 <LIV>
Cross-references: EMBL:L42887; NID:g858715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             279
                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
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               1 CNNSGKDGNAASTNPADESVKGPNLTEISKKITDSNTVVLAVKEVEALLTSIDELATKAI
                               3 CNNSGKDGN-ASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAI 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyme
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease spirochete surface protein
                                                                                                  35.7%;
72.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.8%;
75.6%;
                                                                                     16;
                                                                                Score 642; DB
Pred. No. 5.8e
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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Pred. No. 4.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                  DB 2;
.8e-24;
                                                                                                                                                                                                                                PIDN:AAB37007.1; PID:g1695223
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                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                Length 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 210;
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                                                                                                                                                                                                                                                                                                                                  OspC variation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g1695212
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               60
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                                                                              2:
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A;Molecule type: DNA A;Rosidues: 1-210 <RES: 04281; NID:g434663; PIDN:AAC43297.1; PID:g434664 A;Cross references: EMBL:U04281; NID:g434663; PIDN:AAC43297.1; PID:g434664 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995
                                                                                                                                                                                                                                                                                                                                                            Qy
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Best Local
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R;Stevenson, B.; Barthold, S.W.
FEMS Microbiol. Lett. 124, 367-372, 1994
A;Title: Expression and sequence of outer surface A;Reference number: 140143; MUID:95154673
A;Accession: 140144
A;Status: preliminary; translated from GB/EMBL/DDE
                                                                                                                                        outer surface protein C precursor - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_che C;Accession: I40144; S70282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S70280

R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, Mol. Microbiol. 18, 257-269, 1995

A;Title: Evidence for lateral transfer and recor A;Reference number: S70255; MUID:96296448

A;Accession: S70280

A;Status: nucleic acid sequence not shown
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C;Superfamily: Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:L42868; NID:g858735; PIDN:AAB37011.1; PID:g1695226 A;Experimental source: strain ZS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-193 <LIV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELA-KAIGK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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76.2%;
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Pred. No. 7.2e
16; Mismatches
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.2e-24;
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from GB/EMBL/DDBJ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Molecule type: DNA
A:Residues: 19-210 <LIV>
A:Cross references: EMBL:L42893; NID:g858721;
A:Experimental source: strain 297
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A;Reference number: S70255; MUID
A;Accession: S70282
A;Status: nucleic acid sequence
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A; Residues: 1-152, 'E', 154-211 <ROE>
A; Cross-references: EMBL: X81522; NID: g872021;
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A; Residues: 1-211 <JAU>
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Best Local S
Matches 134
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Best Local Similarity 75.7
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        bmitted to the EMBL Data Library, Reference number: S72674
                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETILLASIDELATKAIGK 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDETKKL 308
              EGEHAQLGIENVTDENAKKAILITDAA-KDKGAAELEKLFKAVENLAKAAKEMLANSVKE
                                                                                                                                                          NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248
                                                         KIKNDGSLGDEANHNESLLAGAYTISTLITQKLSKLNGSEGLKEKIAAAKKCSEEFSTKL
                                                                                               KIOQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL 308
                                                                                                                                      NNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDELA-KAIGK 78
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sequence not shown
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                                                                                                                                                                                                                35.4%; Score 637; DB 2; Length 75.7%; Pred. No. 1.1e-23; tive 17; Mismatches 25; Indel
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Pred. No. 8.4
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C;Accession: I40268
R;Margolis, N.; Hogan, D.; Cieplak, W.
Gene 143, 105-110, 1994
A;Title: Homology between Borrelia burgdorferi OspC
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J. Clin. Microbiol. 31, 2570-2576, 1993
A;Title: Polymorphism in ospC gene of Borrelia burgdorferi
A;Reference number: 140105; MUID:94075528
A;Accession: 140108
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                                                                                    A;Gene: ospC
C;Superfamily: Lyme disease spirochete surface protein
                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-211 <RES>
                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                         outer surface protein C precursor - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
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C;Superfamily: Lyme disease spirochete surface protein
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A; Residues: 1-203 < RES>
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Best Local Similarity
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y Match 34.9%;
Local Similarity 72.8%;
hes 131; Conservative 1
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75.7%;
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; Score 627; DB 2;
; Pred. No. 3.3e-23;
16; Mismatches 33;
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Pred. No. 1.3e-23;
"'~matches 26;
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                                 Length 211
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189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248

Gaps

Search completed: March 18, 2002, 09:56:49 Job time: 372 sec

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Title:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptcdata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*
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US-09-974-992-7
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US-09-915-242-5883
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US-09-708-427-15045
US-09-708-427-15045
US-09-708-427-15044
US-09-708-427-15044
US-09-815-242-5835
US-10-072-851-12996
US-10-072-851-12996
US-10-037-182-8
US-09-938-275-6
US-09-938-275-13883
US-09-708-427-19883
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Compugen
 Sequence
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 75, Appli

58883, Appli

58883, Ap

13080, A

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15044, A

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15046, A

12996, A

12996, A

12996, A

12996, A

1296, A

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RESULT 2 US-09-974-992-7

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GNTSANSA GLAVEAGH SLGDEANH SLGDEANH I LGIQGVTD	larity Conserv	Application Application Application Application Application Mathiesen, Theisen, Holm, Arne Ostergaard VENTION: NO PLICATION NO LICATION LICAT		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
NSGKDGNTSANSADESVKGPNLT IQONGGLAVEAGHNGTLLAGAYT : : : : : :	35. 76. Vative	ition US/09974 ien, Marlanne n, Michael Arne paard, Soren l Novel Ospc- 9-666p 10 2001-10-1 UMBER: 09/18 1999-05-13 1999-05-02 1997-05-02 105: 40 107: 2.1 1097-05-02 1097-05-02 1097-05-02 1097-05-02 1097-05-02		805 841 5795 5795 2056 1043 1043 2076 2186 2186 2186 2186 2186 2186 2186 218
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LTEISKKITDSNAVLLAVKEVEALL YTISKLITQKLDGLKNSEKLKEKIE TISTLITQKLSKLNGSEGLKEKIA YTISTLITQKLSKLNGSEGLKEKIA TDAA-KDKGAAELEKLFKAVENLA :: : :	Score 640; DB 6; Le Pred. No. 8.2e-37; 16; Mismatches 25; ILTEISKKITESNAVVLAVKBIET	9974992 ine J. gpc-derived peptide fragments pC-10 10-10 17180,089 177DK97/00203	ALIGNMENTS	US-09-708-427-3730 US-09-708-427-3729 US-09-815-242-12610 US-10-072-851-12610 US-09-614-150-4824 US-09-708-427-32623 US-09-708-427-32623 US-09-708-427-32623 US-09-815-242-5815 US-10-072-851-5815 US-09-815-242-12913 US-10-072-851-5834 US-10-072-851-5834 US-10-072-851-5834 US-10-073-815-12010 US-09-708-427-15046 US-10-037-182-12 US-09-738-275-7 US-10-037-182-10 US-09-742-096-5 US-10-032-585-7627
FTKKL : : SVKE 	2; Ga KAIGK	. t		Sequence 373 Sequence 372 Sequence 126 Sequence 126 Sequence 326 Sequence 326 Sequence 526 Sequence 581 Sequence 129 Sequence 129 Sequence 583 Sequence 583 Sequence 583 Sequence 150 Sequence 17, Sequence 7, Sequence 70
78 308 138 367 198	1 N B			3730, Ap 3729, Ap 12610, A 12610, A 12624, Ap 32622, A 32

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; ORGANISM: Borrelia garinii
US-09-974-992-3
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LENGTH: 207
TYPE: PRT
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TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-974-992-7
          Matches 118;
                          Query Match
Best Local Similarity
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR APPLICATION NUMBER: PCT/DK97/00203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNA 177
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        Conservative
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  31.5%; Score 567; DB 6; Length 207; 63.1%; Pred. No. 7.8e-32; ative 33; Mismatches 32; Indels
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Pred. No. 2.7e-33;
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US-09-815-242-5883
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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Best Local Similarity
Matches 93; Conserv
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LENGTH: 837
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SOFTWARE: FastSEQ for Window
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
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CURRENT FILING DATE: 2001-03-21
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218 AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 272
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                                                                                                                                                                                                            4 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI----
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                                                                                                                        DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
                                         AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                   DSIANEAT-IKAGQNYTDASQNKQTDYNSAYTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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23.1%; Pred. No. 0.00026;
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US-10-072-851-5883
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LENGTH: 837
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITEA.028A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT FILING DATE: 2002-02-08
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                                                                                                                                                                                                                                                                              100 NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 159
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                                                                                                                                                                                                                        54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
                                                                                                                                                                                                                                                                                                            4 NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI----
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        AVVLAVKEIETLLASIDELATKAIGKKIQQNGGLAVEAG------HNGTLLAGAY 271
                                                                                                                                                          AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
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                                                                                                                          AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN
                                                NADALNTAMTNLKNGIQD-----QNTIKQG-VNFTDADE-----AKRNAYTN
                                                                                    NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN 222
                                                                                                                                                                                                                                                                                                                                                          93;
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Zamudio, Carlos
Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu, H. Howard
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23.1%; Pred. No. 0.00026;
tive 77; Mismatches 154
                                                                                                                                                                                                                                                                                                                                                                                              Length 837;
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SOFTWARE: FastSEQ for
SEQ ID NO 13080
LENGTH: 875
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          Matches
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
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223 AVVLAVKEIETLLASIDELATKAIGKKIQQNGGLAVEAG-----
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                                                                                                                                                                                                                                                                                                            NNSGKDGNASANSADE----SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI---- 53
                                                                                                                          AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI----EGATHVNEVTQAQN
                                                                                                                                                            AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                                                                    DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
                                                                                                                                                                                                                                                                              NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 196
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                                              NADALNTAMTNLKNGIQD-----QNTIKQG-VNFTDADE---
                                                                                    NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN
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                                                                                                                                                                                                                                                                                                                                                          Conservative
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        HNGTLLAGAY 271
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US-10-072-851-13080
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US-10-072-851-13080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
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TYPE: PRT
                       397 TTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQVSTTASELNTAMSNLQNGINDEAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  137 NHNLEVAKQNANTAIDGLTSLNGPQKAKLKEQVGQATTLPNVQTVRDNAQTLNTAMKGLR 196
                                                             272 TISKLITOKLDGLKNSEK--LKEKIENAKK---CSEDFTKKLEGEHAQLGIEN-VTDENA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 NNSGKDGNASANSADE---SVKGPNLTEISKKITESNAV--VLAVKE-VETLLASI---- 53
                                                                                                                                              AVVLAVKETETLLASIDELATKATGKKIQQNGGLAVEAG-----
                                                                                                                                                                                        NADALNTAMTNLKNGIQD-----QNTIKQG-VNFTDADE-----AKRNAYTN
                                                                                                                                                                                                                              NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN 222
                                                                                                                                                                                                                                                                     AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 309
                                                                                                                                                                                                                                                                                                             AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                                                                                                                                                                                                                   DSTANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T
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                                                                                                       AVTQA-------EQILNKAQGPNTSKDG---VETALENVQRAKNELNGNQNVANAK
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Ohlsen, Kari L
Zyskind, Judith W.
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                                                                                                                                       RESULT 9
US-09-708-427-15044
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LOCATION: 1..1304
COTHER INFORMATION: Ceres Seq.
US-09-708-427-15045
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US-09-708-427-15045
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                                                                                                   Sequence 15044, Application US/09708427 GENERAL INFORMATION:
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LENGTH: 1304
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Best Local :
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APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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OTHER INFORMATION: Xaa
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nes 91; Conserv
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NUMBER: US/09/708,427
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Pred. No. 0.0012;
10; Mismatches 136; Indels
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                                                             DNA FRAGMENTS AND CORRESPONDING
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; LOCATION: 1..1313
; OTHER INFORMATION: Ceres
US-09-708-427-15044
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NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15044
LORGH: 1313
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                    TITLE OF INVENTION: Identification of Essential Ge TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITA.011A

CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727
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Best Local S
Matches 91
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APPLICANT:
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OTHER INFORMATION: Xaa is any amino acid
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Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                  Wall, Daniel
Trawick, John D.
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22.8%; Pred. No. 0.0012;
tive 80; Mismatches 136; Indels 9
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; APPLICANT: Jiang, Borne; APPLICANT: Boone, Charles; APPLICANT: Bussey, Howard; TITLE OF INVENTION: Methods for Identifying th; TITLE OF INVENTION: Proliferation
: FILE REFERENCE: ELITAR.028A; CURRENT APPLICATION NUMBER: US/10/072,851; CURRENT FILING DATE: 2002-02-08
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US-10-072-851-5835
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Best Local S
Matches 94
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5835
LENGTH: 2434
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5835,
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APPLICANT:
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Carr, APPLICANT: Xu, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 KKAI-LITDAAKDKGAAELEKLFKAVENLAKAA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVTQA-----EQILNKAQGPNTSKDG---VETALENVQRAKNELNGNQNVANAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVVLAVKEIETLLASIDELATKAIGKKIQQNGGLAVEAG------HNGTLLAGAY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQVSTTASELNTAMSNLQNGINDEAA 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN 222
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94; Conserv
                                                                                                                                                                                                                                             Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                Yamamoto, Robert T. Roemer, Terry
                                                                                                                                                                                                   Trawick, John D.
                                                                                                                                                                                                                          Wall, Daniel
                                                                                                                                                                                                                                                                                      Haselbeck, Robert
                                                                                                                                                                                                                                                                                                       Foulkes, J. Gordon
Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                 Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                           Application
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                                                                                                                                                                                                                                                                                                                                                                      Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.4%; Score 169.5; DB 6; 23.9%; Pred. No. 0.0029; ative 76; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60/242,578
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                                                                                   Compound which Inhibit
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US-09-815-242-12996
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US-10-072-851-5835
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LENGTH: 2434
                                                             PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                         PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/267, PRIOR FILING DATE: 2001-02-09 NUMBER OF SEQ ID NOS: 15811
                    PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                  PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quence 12996, Application US/09815242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 9.4%;
Local Similarity 23.9%;
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APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind, Judith W. Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                        Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant J.
Yamamoto, Robert T.
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US-09-815-242-12996
                               APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA,028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-072-851-12996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12996
SEQ ID NO 12996
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Best Local
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                     SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 TISKLITQKLDGLKNSEK--LKEKIENAKK---CSEDFTKKLEGEHAQLGIEN-VTDENA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 DELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAE----KLNVLKNEELKEKIDT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 1653
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                                                                                                                                                                                                                                                             Trawick, John D.
Yamamoto, Robert
Roemer, Terry
                                                                                                                                                                                                                                                                                                                             Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                           Foulkes, J. Gor
Zamudio, Carlos
                                                                                                                                                                                                                         Boone, Charles
                                                                                                                                                                                                                                                                                                                                                  Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck, Robert
                                                                                                                                                                                                                                            Jiang, Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10072851
                                                                                                                                                                                                                                                                                                                                                                                                                                                 H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grant J.
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                                                                                                                                                                                                                                                                                       Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon
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                                                                                                                                                                                 Identifying
                                                                                                                                                                                   the
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                                                                                                                                                                                   Compound which
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                                                                                                                                                                                   Inhibit
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. NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1765
TYPE: PRT
ORGANISM: Homo sapiens
US-10-037-182-8
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US-10-037-182-8
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/037,182
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,449
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/279,282
PRIOR FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thyboll, Jill
TITLE OF INVENTION: Recombinant Laminin 10
FILE REFERENCE: 99-274-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tryggvason, Karl APPLICANT: Doi, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1599
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                                                                                  1384
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1444 VSEAKLRAD------EAKQSAEDILLK----TNATKEKMD-KSNEELRNLIKQIRN 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1654 NADALNTAMTNLKNGIQD------QNTIKQG-VNFTDADE-----AKRNAYTN 1694
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                                                                                                                                                                                   Local Similarity 24.6%;
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                                                                                                                        2 ACNNSGKDG-NASANSADESVKGPNLTEI-----SKKITESNAVVLAVKEVETLLAS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAKNALNNLTSINNAQKEALKSQIEGATTVAGVNQVSTTASELNTAMSNLQNGINDEAA 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSIANEAT-IKAGQNYTDASQNKQTDYNSAVTAAKAIIGQTTSPSMNAQEINQAKDQV-T 1598
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                                      IDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQ 112
                                                                               SCSETECGGPNCRTDEGERKCGGPGCGGLVTVAHNAWQKAMDLDQDVLSALAEVEQLSKM 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKAI-LITDAAKDKGAAELEKLFKAVENLAKAA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLS--KAAQDTLKNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTEISKKITESN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKQQALNGQENLRTAQTNAKQHLNGLSDLTD--AQKDAVKRQI---EGATHVNEVTQAQN 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKQCSTEFTNKLK-----SEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVE 164
                                                                                                                                                                    102;
                                                                                                                                                                    Conservative
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                                                                                                                                                                 61;
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Pred. No. 0.0023;
1; Mismatches 160;
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                                                                                                                                                                 Indels 91;
                                                                                                                                                                                                      Length 1765;
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P07942
; DATABASE ENTRY DATE: 1988-08-01
US-09-938-275-6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Therapeutic and Diagnostic Applications TITLE OF INVENTION: of Laminin and Laminin-Derived Protein FILE REFERENCE: PROTEO.P03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/938,275
CURRENT FILING DATE: 2001-08-16
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1673 EKVV---YTVKQSAEDVKKTLDG-ELDEKYK-KVENLIAKKTEESADARRKAEMLQNEAK 1727
                                                                                                                                                                                                                                                                                    1510 FLTQDSADLDSIEAVANEVLKMEMPSTPQQLQNLTEDIRERVESLSQVEVILQHSAADIA 1569
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                                                                                                                                                                                                                                    153 AAELEKLEKAVENLSKAAQDT-----LKNAVKELTSPIVHGNNSGKDGNTSANSADESV
                                                                                                                                                                                                                                                                                                                                 113 CSTEFTNKLKSEHAVLG------LDNLTDDNAQRA-----ILKKHANKDKG 152
                                                                                                                                                                                                                                                                                                                                                                                                                          53 IDELATKAIGKKIGNNGLEANOSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKO 112
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                                          GTLLAGAYTISKL---ITQKLDGLKNSEKLKEKIEN--AKKCSEDFTKKLEGEHAQLGIE 318
                                                                                                                         KGPN--LTEISKKITESNAVVL-AVKEIETLLASIDELATKAIGKKIQQNGGLAVEAGHN 263
                                                                                                                                                                                        RAEM--LLEEAKRASKSATDVKVTADMVKEALEEAEKAQVAAEKAIK-----QADEDI 1620
                                                                                                                                                                                                                                                                                                                                                                                VSEAKLRAD --
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                                                                                            QGTQNLLTSIESETAASEETLFNASQRISELERNVEELKRKA-----AQNSG---EAEYI 1672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 168.5; DB 5; 24.6%; Pred. No. 0.0023;
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Search completed: March 18, 2002, 09:58:33 Job time: 391 sec

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EMBL; U01894;
EMBL; D49497;
      "Molecular analysis and expression encoding a 22 kDa protein (pC) in F Mol. Microbiol. 6:503-509(1992).
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Bacteria; Spirochaetales; S
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nature 390:580-586(1997).
-!- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
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ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1
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                                           of a Borrelia burgdorferi gene
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EMBL; X73624; CAA52003.1; -.
EMBL; X73624; CAA52003.1; -.
EMBL; X73624; CAA52003.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein; Signal; Plasmid; Antigen.
Outer membrane; Lipoprotein; Signal; Plasmid; Antigen.
BY SIMILARITY.
OUTER SURFACE PROTEIN C.
OUTER SURFACE PROTEIN C.
N-ACYL DIGLYCERIDE (BY SIMILARITY).
                                                                                                                                                                               01-OCT-1993
01-OCT-1993
01-FEB-1994
STRAIN-SSP, HS1 SEROTYPE 24;
STRAIN-SSP, HS1 SEROTYPE 24;
MEDLINE-93133110; PubMed=1484486;
Restrepo B.I., Kitten T., Carter C.J.,
"Subtelomeric expression regions of Boj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theisen M., Frederiksen B., Lebech A.M., Vuust J., Har Polymorphism in ospC gene of Borrelia burgdorferi and immunoreactivity of OspC protein: implications for tause of OspC protein as a diagnostic antigen.";
J. Clin. Microbiol. 31:2570-2576(1993).
-i- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
                                                                                                                                                                                                                           VM24_BORHE
P32778;
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SEQUENCE OF 1-205 FROM N.A.
STRAIN-DK26;
MEDLINE-94075528; PubMed-8253951;
                                                                                                     Bacteria;
                                                                                                                      Plasmid
                                                                                                                                      Borrelia hermsii
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                                                                                                                                                                 MAJOR
                                                                                                     Spirochaetales;
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el. 27, Last sequence up
el. 28, Last annotation
OUTER MEMBRANE LIPOPROT
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68.8%;
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                                                                                                       Spirochaetaceae;
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); Mismatches
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No. 1.7e-20;
 Borrelia hermsii linear
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SEQUENCE
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Plasmid.
are highly polymorphic.",
Mol. Microbiol. 6:3299-3311(1992).
-i-FUNCTION: SERVES TO AVOID THE |
FROM ONE SURFACE EXPOSED VMP To
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                                                                       STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
                                                                                                                                                           Borrelia
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                                                "Subtelomeric expression regions
                                                                                                  SEQUENCE FROM N.A
                                                                                                                                    Bacteria; Spirochaetales;
                                                                                                                                                                                    VARIABLE
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Microbiol. 6:3299-3311(1992).
FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE BY CHANGING FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPII
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(Rel. 28,
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                                                C.J., Infante D., Barbour i
of Borrelia hermsii linear
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Matches 80
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01-MAY 1992 (Rel. 22, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
INTRACELLULAR PROTEIN TRANSPORT PROTEI
USO1 OR INT1 OR YDL058W.
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                                                                                                                                                                                                                                                        Nakajima H., Hirata
Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1
      Submitted
                                                                                                                                                                                                                                                                                  MEDLINE-91185402; PubMed-2010462; Nakaiima H., Hirata A., Ogawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P25386;
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                                       Kendrick K.E.
                                                                 Hostetter M.
                                                                                                  SEQUENCE OF
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80; Conservative
                                                                                                                                                            transport in Saccharomyces Biol. 113:245-260(1991).
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215 i
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18 PROBABLE.
215 VARIABLE MAJOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD
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      EMBL/GenBank/DDBJ databases
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T PROTEIN USO1.
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                                                                 McClellan M.,
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Bai Y., Symington L.S.;
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Submitted (MAY-1996) To the
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EMBL; L03188; AAB00143.1;
EMBL; U53668; AAB66659.1;
PIR; A38455; A38455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                        ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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SGD; S0002216; USO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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           211 LTEISKKITESNAVVLAVKETE
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                                                                                                                                                                                                                                                                                                                          ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACE MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEE ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CO OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: REQUIRED COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                               EEIISKSDSSKDEYESQISLLKEKLETATTANDENVNKISELTKTREELEAELAAYKNLK 1098
                                                                                                                                                                                                                      E------VETILASIDELATKAIGKKIGNNGLEAN--QSKNTSLLSGAYAISDLIAEK 94
                                                                                                                                                                                                                                                        CNNLSKEKEHISKELVEYKSRFQSHDNLV--AKLTEKLKSLANNYKDMQAENESLIKAVE 986
                                                                                                                                                                                                                                                                                     CNNSGKDG-----NASANSADESVKGPNLTEISKKI-----TESNAVVLAVK 44
                                    AQLKKYEEQIANKERQYNEEISQLN----
                                                                                           NELETKLETSEKALKEVKENEEHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHEDLA 1158
                                                                                                                      -----TDDNAQRAI------LKKHANKDKG-----AAELEKLFKAVENLS 167
                                                                                                                                                                                                    ESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIEKNIEQLKKT-----ISDLEQTK 1038
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CHARGED (HYPER-HYDROPHILIC).

CHARGED (HYPER-HYDROPHILIC).

DISPENSABLE FOR THE PROTEIN FUNCTION.

ASP/GLU-RICH (ACIDIC).

G -> E (IN REF. 2).

E -> K (IN REF. 2).

V -> I (IN REF. 2).

I -> V (IN REF. 2).

I -> V (IN REF. 2).

G -> S (IN REF. 2).

G -> S (IN REF. 2).

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I -> V (IN REF. 2).

G -> S (IN REF. 2).

G -> S (IN REF. 2).

C -> D -> DEEDDEE (IN REF. 2).

C -> CEZB216E9FD4818 CRC64:
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Pred. No. 0.51
66; Mismatches
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            -TLLASIDELATKAIGKKIQQNGGLAVEAGH 262
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MEDLINE=99120557; PubMed=9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.

Raith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Tves C.,

Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,

Tummino P.J., Caruso A., Uria-C. Tiang O., Taylor D.E., Vovis (
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYTOTOXICITY ASSOCIATED IMMUNODOMINANT ANTIGEN
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CAGA OR CAI OR CAG26 OR JHP0495.
Helicobacter pylori J99 (Campylobacter pylori J99)
Bacteria; Proteobacteria; epsilon subdivision; Hel
                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence comparison of two unrelated isolates of gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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                                                            SVAKATGDFSG---VEQALADLKNFSKEQLAQQAQKNEDFNTGKNSA----LYQSVKNGV
                                                                                             ----CSTEFTNKLKSEHAVLGLDNLTDDN-AQRAILKKHANKDKGAAELEKLFKAVEN--
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NGTLVGNGLSKAEATTLSKNFSDIKKELNAKL--GNFNNNNNNGLENSTE---
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                            ----LSKAAQDTL----KNAVKELTSPIVHGNNSGKDGNTSANSADESVKGPNLTE 213
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                                                                                                                             ----KNGKNKDFSKVTQ-----AKSDLENSIKDVIINQKITDKVDNLNQAV 795
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Pred. No. 0.
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RESULT
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01-AUG-1988 (Rel. (
20-AUG-2001 (Rel. 4
LAMININ BETA-1 CHA)
      Am. J. Hum. Genet. 41:605-615(1987).

Am. J. Hum. Genet. 41:605-615(1987).

IF FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

INTERPRITE POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPAISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-1 (BESTA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-2 (MEROSIN), AND LAMININ-6 (K-LAMININ).

INTERPRITE SUBCELPULAR LOCATION: EXTRACELPULAR.

INTERPRITE SUBCELPULAR LOCATION: EXTRACELPULAR.

INDOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

INDOMAIN: DOMAINS VI AND LY ARE GLOBULAR.

INDOMAIN: DOMAINS VI AND LY ARE GLOBULAR DOMAIN (DOMAIN VI).

INSIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
NCBI_TaxID=9606;
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Mammalia; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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J. Biol. Chem.
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                                                                                                                                                                                                                                                                                                                           Isolation of a cDNA clone for the human laminin-Blene localization.";
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(LAMININ B1 CHAIN).
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EMBL; M61951; M58147; M55359; M55360; M55361; M55362; M55363; M55364; M55366; M55367; M61935 м61933; M61932 M61930 M55355 M55373 M61938 AAA59486.1; AAA59486.1; AAA59486.1; AAA59486.1; AAA59486.1; AAA59486.1; AAA59486 AAA59485 AAA59486. AAA59486. AAA59486. JOINED
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PRINTS; PROUD1; EGFLAMININ
PRODOM; PROUD2082; LAMNT; 1.
SMART; SMO01360; EGF_LAM; 11.
SMART; SMO0136; EMINT; 1.
SMART; SMO0136; LAMNT; 1.
PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 2.
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InterPro; IPR001886; LamNT.
InterPro; IPR002049; Laminin_EG
Pfam; PF00053; Laminin_EGF; 13.
Pfam; PF00055; Laminin_Nterm; 1
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MIM; 150240;
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M61916;

M20206;

S13547; N
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AAA59482.1;
AAA59487.1;
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EGF-LIKE
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W EGF-LIKE 4.
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W EGF-LIKE 5.
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(POTENTIAL).
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RX MEDLINE-2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basch R.G., Letter G., Helt G., Walson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Bascu A., Baxendale J., Bayraktarroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugann Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Ephydroidea; Drosophilidae; Drosophila.
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Melson K.A., Nixon K., Nusskern D.R., Pelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeben Y.H., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
RI Sclence 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caggese C., Ragone G., Perrini B., Moschetti R., de Pil Caizzi R., Barsanti P.;
"Identification of nuclear genes encoding mitochondria: isolation of a collection of D. melanogaster cDNAs home sequences in the Human Gene Index database.";
HOL. Gen. Genet. 261:64-70(1999).
-I- SUBCELLULAR LOCATION: TOCHONDRIAL.
-I- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOM.
-I- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUI FRAMESHIFTS IN POSITIONS 920 AND 930.
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PF01334;
PF02721;
PF00036;
PF02185;
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IPR002024; Bacterioferritin.
IPR003871; DUP223.
IPR002048; EF-hand.
IPR002048; EF-hand.
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RESULT 9
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           Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du i A Favello A., Fulton L., Gattung S., Greco T., Kirsten J., A Favello A., Fulton L., Gattung S., Greco T., Kirsten J., A Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., A Johnson D., Johnston L., Langston Y., Latreille P., Le T., A Johnson D., Johnston L., Langston Y., Latreille P., Le T., A Marcis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso I A Milcox L., Wohldman P., Vaudin M., Wilson R., Waterston R., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: ESSENTIAL COMPONENT OF THE NUCLEOSKELETON. POTEI CROCKEL IN CROSSLINKING FILMENTS OR ANCHORING OTHER MOLECULI IS ESSENTIAL FOR GROWTH.
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Best Local
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01-OCT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN
NUF1 OR SPC110 OR YDR356W OR D9476.3.
                                                                                                                                                                                                                                                                               Kilmartin J.V., Dyos S.L., Kershaw D., Finch J.T.;
"A spacer protein in the Saccharomyces cerevisiae spindle poly body
whose transcript is cell cycle-regulated.";
J. Cell Biol. 123:1175-1184(1993).
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"The NUF1 gene encodes an essential coiled-coil related is a potential component of the yeast nucleoskeleton.";
J. Cell Biol. 116:1319-1332(1992).
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NCBI_TaxID-4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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LL; X73297; CAA51733.1; -.

IL; UZ8372; AA864791.1; -.

IL; S26710; S26710.

IL; S34288; S34288.

IL; S34288; S34288.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
100; Conser
                                          -2001 (Rel. 40, Last annotation update) (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).
gallus
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(Rel. 36, Last sequence update)
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                                                                                                                                          STANDARD; P
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NUCLEAR LOCALIZATION INUCLEAR LOC
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Pred. No. 1;
71; Mismatches
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N; 04FAA074BB8A0BC8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed predominantly in muscle.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEEMS TO BE A INVERNEDIATE FILAMENT ASSOCIATED PROTE:
-!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
--- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
CYTOSKELETON (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED BY
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00343; ZnF_C2HC; PROSITE; PS00845; CAP_GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF014012; AAC60344.1; -. EMBL; AF020764; AAC60345.1; -. EMBL; AF045650; AAC03547.1; -. EMBL; AF045551; AAC03548.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=98137792; PubMed=9469933;

Griparic L., Volosky J.M., Keller T.C.

"Cloning and expression of chicken CLII

Gene 206:195-208(1998).
                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000938; CAP-Gly.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF01302; CAP_GLY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Griparic L., Keller T.C. III; "Identification and expression of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
127
                              561
                                                                                                                                                                                                                                                                                                                                                                                     NIAMOC
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                                                                                           508
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                                                                                                                    18 DESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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VLGLDNLTDDNAQRAILKKHANKDKGA--AELEKLFKAVENLSKAAQDTLKN---
                            SSLKEKFESSEEALRKEIKTLSASNERMGKENESLKTKLDHANKENSDVIELWKSKLESA
                                                                                        DLALRVKEVAELRGRLESSK----HIDDVDTSLSLLQEIS--SLQEKMAAAGKE-HQREM 560
                                                                                                                                                 Similarity 22.5
86; Conservative
                                                                                                                                                                                                                                                                                         803
458
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22.5%;
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K -> R (IN REF. 2; AAC
E -> V (IN REF. 2; AAC
MW; 5631CE8683498E23 C
                                                                                                                                                                                                                              MW;
                                                                                                                                                 Score 158.5;
Pred. No. 2.2;
78; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil;
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CCHC-BOX.
MISSING (IN SHORT ISOFORM).
TOTKLEHARIKELEQSLLFEKTKADKLQRELEDTR ->
TOTKLEHARIKELEQSLLFEKTKADKLQRELEDTR ->
                                                                                                                                                                                                                                                                                      RKRQISEDPEN (IN ISOFORM CLIP-170(11)).

S -> GGSSKVS (IN ISOFORM CLIP-170(11)).

T -> RKRQISEDPENT (IN ISOFORM CLIP-
                                                                                                                                                                                                                                                                                                                                                                                                   SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                CAP-GLY 2.
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                                                         -KNEELKEKIDTAKQCSTEFTN--KLKSEHA 126
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CLIP-170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splicing
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. 2; AACO3548).
498E23 CRC64;
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Best Local
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                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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Bacteria; Proteobacteria; epsilon subdivision;
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35, Last sequence update)
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                                   EK - - SLKKREHLEKGDVAKNLESKSGNKNKMEAK -
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01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                         the European Bioinformatics Institute. There are no use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86111835; PubMed-3511046; MEDLINE-8611835; PubMed-3511046; Tischetti V.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCOTT J.R., Pulliam W.M., Hollingshead S.K., Fischetti V.A.;
"Relationship of M protein genes in group A streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 82:1822-18826(1985).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPES
OF PROTEIN M. PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF
                            Pfam; PF00746; Gram_pos_anchor; Pfam; PF02370; M; 9.
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                                                                        InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
                                                                                                                                   PIR; A26297; A26297
                                                                                                                                                          EMBL; M11338;
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SIMILARITY: TO OTHER STREPTOCOCAL AND
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01-APR-1993
01-OCT-1996
  SEQUENCE FROM N.A.
MEDLINE-92315338; PubMed-1617731;
Galinski M.R., Medina C.C., Ingra-
"A reticulocyte-binding protein co
                                                          Eukaryota;
                                                                                                                         RBP2_PLAVB
Q00799;
                                                 NCBI_TaxID=31273;
                                                                  Plasmodium vivax
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                                                                                                                                                                                                                                                                     DELATKAIGKKIQQNGGLAVEAGHNGTLLAGAYTISKL--ITQKLDGLKNSEK---
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                                                                                                                                                                                                                                                                                                          GNTSANSADESVKGPNLTEISKKITESNAVVLAVKEI--ETLLASI-------
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                                                                                                                                                                                                                                                                                                                                                                                                      LNKYDVENSMLQANNDKLTTE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MAKNNTNRHYSLRKLKKGTASVAVA-LSVIGAGLVVNTNEVSARVFPRGTVENPDKAREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                     BINDING
                                                                                                                                  STANDARD;
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                                                                          . 25, Created)
. 25, Last sequence update)
. 34, Last annotation update
. 34 protein 2 (FRAGMENT).
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24.8%;
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  .C., Ingravallo P., protein complex of
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GLY/PRO-RICH (CELL WALL-SPACONSERVED IN GRAM-POSITIVE
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68F87F28DB53A448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 x 7 AA TANDEM REPEATS.
4.5 x 25 AA TANDEM REPEATS.
TWO DIRECTLY REPEATED 27 AMINO ACID
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EXTRACELLULAR (POTENTIAL).
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                                                        Haemosporida;
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008696;
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01-FEB-1995
20-AUG-2001
                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                      MST101(2).
Drosophila hydei (Fruit fly)
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NON_TER
SEQUENCE
NCBI_TaxID=7224;
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Cell 69:1213-1226(1992).

-i- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECHUMAN RETICULOCYTE CELLS.

-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              TDA----AKDKG-----
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                                                                                         (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
^^rameD PROTEIN MST101(2).
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AA; 143741 MW;
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21.3%;
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RESULT 15
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Eur. J. Biochem. 225:1089-1095(1994).
Eur. FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               motif representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely elongated spermatozoa of
MYSN_DROME Q99323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL
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                                                                                                                                                                                                                                   AVKEIETLLASIDELATK-----AIGKKIQQNGGLAVEAGHNGTLLAGAYTISKLITQKL
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                                                                                      AAKKEKEAAEREKCGELAKKIKKAAEKKKCKKLAKKEKE
                                                                                                                 -AAKDKGAAELEKLFKAVENLAKAAK----EMLANSVKE
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                                                                                                                                                                                                                                                                EAAERKKCEELAKKIKKAAEKKKCEET-AKKGKEVAERKKCEELAKKIKKAEIKKKCKKL
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Repeat; Multigene family; Polymorphism.

32 1268 59 X 16 AA APPROXIMATE TANDEM REPEATS

[KR]-K-X-C-X-X-X-K-X-X-K-X-X-X-X-E.

4 391 AA; 159000 MW; 1B2A36BF30F48878 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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               STANDARD;
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27.3%;
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Pred. No. 2.
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Matches 91
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InterPro; IPR002928; Myosin_tail.
InterPro; IPR002928; Myosin_head.
InterPro; IPR001609; Myosin_head;
Pfam; PF00612; IQ; 1.
Pfam; PF00063; Myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRIMTS; PR00193; MYOSINLBAVY.
PRODOM; PD000355; MYOSIN_head; 1.
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Eukaryota; Metazoa; Arthropoda; Tracheata; He Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
MCBI_TaxID=7227;
                                                                                                             VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
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MEDLINE=90349606; PubMed=2117279;
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B36014; B36014.
                       Similarity
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                    Score 155.5;
Pred. No. 4.
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MISSING (IN SHORT )
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ALPHA-HELICAL TAILPIECE (LMM).
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50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING
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; Tracheata; Hexapoda; Insecta;
; Tracheata; Brachycera; Muscomorpha;
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tail and differential
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127 VLGLDNLTDDNAQRAILKKHAN-------KDKGAAELEKLFKAVENLSKA------AQD 172
122 TL------KRSLEEETVNHEGVLADMRHKHSQELNSINDQLENLFKAKTVLEKAKG 1271
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                                                                                                                                                      1327 TKLQQEAENITNQL-EEAELKASAAVKSASNMESQLTEAQQLLEEETRQKL-GLSSKLRQ 1384
                                                                                                    287 ----SEKLKEKIENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAE 342
                                                                                                                                                                                        233 TLLASIDELATKAIGKKIQQNGGLAVEAGHN--GTLLAGAYTISKLITQKLDGLKN---- 286
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Search completed: March 18, 2002, 10:11:57 Job time: 975 sec

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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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sp_unclassified:*
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sp_virus:*
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0.4RR52
0.9S3P1
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borrelia
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ja	borrelia	P96571	P96571	N	201	4	.8	5
af	borrelia	Q9kim5	Q9KIM5	N	212	٠.	ω.	4
af	borrelia	050624	050624	N	203	4.		
nq	borrelia		050619	N	203	4.		
ņ	borrelia	P94236	P94236	N	193		625	
	borrelia	031121	031121	N	184	٠.	626	
	borrelia	4976	Q44976	N	211	٠.	627	
	borrelia	r7b2	Q9R7B2	N	182	ŗ	628.5	
	borrelia	xdh4	Q9XDH4	N	200	Ģ	629	
	borrelia		P96516	Ŋ	201	5	629.5	
	borrelia	6514	P96514	N	201	5	ŭ	
ğ	borrelia	1114	031114	N	194	5	630	
þ	borrelia	034124	034124	N	181	5	634	
ja		P96573	P96573	Ŋ	201	5	634.5	
nd	borrelia	8138	Q08138	N	203	5	635	
ja	borrelia	6572	P96572	Ŋ	201	5	Ψ	
nq	borrelia	P70818	P70818	N	191	35.5	637.5	29
nq	borrelia	4719	Q44719	N	210	5	ω	
nq	borrelia	Q9s3p2	Q9S3P2	N	192	ŗ	ω	
nd	borrelia		Q44977	N	211	<u>ب</u>	640	
ď	borrelia		P94242	N	193	<u>ب</u>	640	
ď	borrelia		Q9S504	ພ	184	5	640	
ņ	borrelia		031120	N	191	5	640.5	
ņ	borrelia		Q9XDH3	N	188	5	641	
'n	borrelia		P94237	N	193	5	642	
ğ	borrelia			2	200	ŗ	644.5	

ALIGNMENTS

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Qy 121 LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180	OY 61 IGKKIGNNGLEANOSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKOCSTEETNK 120	QY 1 MACNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKA 60 ::	Query Match 50.1%; Score 901; DB 2; Length 192; Best Local Similarity 98.9%; Pred. No. 2.8e-35; Matches 184; Conservative 2; Mismatches 0; Indels 0; Gaps	FT NON_TER 192 192 SQ SEQUENCE 192 AA; 20555 MW; FF16D409D58C01C5 CRC64;	DR ProDom; PD001149; Lipoprotein_6; 1. FT NON_TER 1 1		RL Genetics 151:15-30(1999).	"Genetic diversity of ospC in a local population of Borrelia	RA Wang I.N. Dykhuizen D.E. Olu W. Dunn J.J. Bosler E.M. Luft B.J.:		RN [1]		OUTER SURFACE PROTEIN C	DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	01-MAY-2000 (TrEMBLrel. 13,	ID O9RR52 PRELIMINARY; PRT; 192 AA. AC O9RR52;	RESULT 1
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Best I
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     SEQUENCE FROM N.A.
STRAIN-28691;
MEDLINE-96296448; PubMed-8709845;
MAYON I., Glbbs C.P., Schuster R.,
Evadance for lateral transfer and
                                                                                                                      Q9S3P1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update
01-JUN-2001 (TrEMBLrel. 17, Last annotation update
01-TUN-2001 (TrEMBLrel. 17, Last annotation update
01-grace protein C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borre
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EMBL; U04240; AAC45538.1; (
EMBL; U04240; AAC45538.1; (
InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 209 AA; 22393 MW; 3707A47DAA736FCA CRC64;
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01-NOV-1996
01-JUN-2001
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"Expression and gene sequence of outer surface public procession and gene sequence of outer surface public procession and gene sequence of outer surface public processions."
                                                                                                                NCBI_TaxID=139;
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NCBI_TaxID=139;
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Pred. No. 3.1e-35;
2; Mismatches 0;
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RT DR DR FT FT SQ
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Best Local
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031117;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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NON_TER
SEQUENCE
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Wang I.-N., Dykhuizen D.E., Dunn J.J., Luft B.
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ
EMBL; AF029866; AAB86549.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OUTER SURFACE
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD0001149; Lipoprotein_6; 1.
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EMBL; L42894; AAB37002.1; -.
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                                                                                                           3 CNNSGKDGNASANSADESVKGPNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIG
           LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE 180
                                                                    IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNYLKNEELKEKIDTAKQCSTEFTNK 120
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LKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKE
                                                     IGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNK
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
CE PROTEIN C (FRAGMENT).
                                                                                                                                                                   Conservative
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Spirochaetaceae; Borrelia.
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Pred. No. 1e-34;
2; Mismatches
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Best Local Similarity
Matches 180; Conserv
Wang I. N., Dykhuizen D.E., Dunn J.J

Submitted (OCT-1997) to the EMBL/Gen

EMBL; AF029871; AAB86554.1;

InterPro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.
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Mol. Microbiol. 18:257-269(1995).
EMBL; L42895; AAB37003.1;
InterPro; IPRO01800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lymu
Bacteria; Spirochaetales;
NCBI_TaxID=139;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
00-JUN-2001 (TREMBLREL). 17, Last annotation updat
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Livey I., Gibbs C.P., Schuster R.,
"Evidence for lateral transfer and
                                                                                                                                                                                                                STRAIN-OC12;
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                                                                                                                                              Dunn J.J., Luft B.J.;
EMBL/GenBank/DDBJ dat
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01-MAY-2000 (TrEMBLrel.
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Pfam; PF01441; Lipoprotein_6; 1.
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Bacteria; Spirochaetales;
CBI_TaxID=139;
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                                                                                                                                                                                                  KIQQNGGLAVEAGHNGTLLAGAYTISKLITQKLDGLKNSEKLKEKIENAKKCSEDFTKKL
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194
194
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nilarity 100.0%;
Conservative 0
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nilarity 100.0%;
Conservative
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                        PRELIMINARY;
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194
20640 ⊁
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Lipoprotein_6;
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21457
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    Created)
    Last sequence update)
    Last annotation updat
    PRECURSOR (FRAGMENT).

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        Score 876; I
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                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          806F198295101B07 CRC64;
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                        191
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031123
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Best Local S
Matches 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O31123 PRELIMINARY; PRT; 185 AA.
O31123;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence up
O1-JUN-2001 (TrEMBLrel. 17, Last annotation
OUTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                      wang I.N., Dykhuizen D.E., Dunn J.
submitted (CCT-1997) to the EMBL/Gei
EMBL; AF029872; AAB86555.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fung B.P., McHugh G.L., Leong J.M., Steere A.C.;
"Humoral immune response to outer surface protein C of Borrelia burgdorferi in Lyme disease: role of the immunoglobulin M response the serodiagnosis of early infection.";
Infect. Immun. 62:3213-3221(1994).
EMBL; U08284, AAA2146.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
189 NNSGKDGNTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OC13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-UNV-2001 (TIEMBLIEL 17, Last annotation update)
00TER SURFACE PROTEIN C (FRAGMENT).
BOTTELIA DUTGGOTFETI (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrel.
NCBI_TaxID-139;
                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94314437;
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nes 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 178; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLAKAAKEMLANSVKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185
185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AA;
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=8039891;
                                                                                                                                                                                                        185
19673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20150 MW; C49A4030F0A28717 CRC64;
                                                                                                    46.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e disease spiroch
Spirochaetaceae;
                                                                             Score 841; DE
Pred. No. 1.6e
2; Mismatches
                                                                             2.
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Pred. No. 1.6e-33;
D; Mismatches 1
                                                                                                                                                                                                   58D6FEE3C7769CAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spirochete).
                                                                  DB 2,
1.6e-32;
2;
                                                                                                                                                                                                                                                                                                                                                                                                    Luft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                        Length
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                                                                             Indels
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                                                                             Gaps
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RESULT Q44979
ID 979
ID 979
ID 979
ID 011
DT 011
DT 011
DT 011
DT 020
GN 055
OS Bc
OS Bc
OX NC
STRP STERM
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Q 2439L7
Q 2439L7
Q 2439L7
Q 2439L7
Q 2539L7
Q 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sin
Matches 171;
                                                                                                                                                                                                  Q44979
Q44979;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                    Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; SCBI_TaxID=139;
                                                                                                                                                          OSPC
                                                                                                                                                                           01-NOV-1996 (TremBLrel.
01-JUN-2001 (TremBLrel.
OUTER SURFACE PROTEIN C
STRAIN=272;
MEDLINE=95286481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; P
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         044995;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-JUN-2001 (TrEMBLrel. 17, Last annotatio
OUTER SURFACE PROTEIN C (FRAGMENT).
                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Evolution of the Borrelia burgdorferi outer surface J. Bacteriol. 177:3036-3044(1995).

EMBL; X84779; CAA59250.1; -.

Interpro; IPR001800; Lipoprotein_6.

Pfam; PF01441; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSPC.
Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95286481;
Theisen M., Borre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q44995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 NTSANSADESVKGPNLTEISKKITESNAVVLAVKEIETLLASIDELATKAIGKKIQONGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130
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(TIEMBLIEL 01, Last sequence up
(TIEMBLIEL 17, Last annotation
DE PROTEIN C (FRAGMENT).
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98.8%;
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.8e-32;
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Best Local Sin
Matches 154;
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Best Local Similarity
Matches 170; Conserv
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NON_TER
SEQUENCE
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EMBL; X84782; CAA59253.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein 6: 1
NON_TER
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SEQUENCE
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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J. Bacteriol. 177:3036-3044(1995).
EMBL; X84785; CAA59256.1; -
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Bacteria; Spirochaeta
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nilarity 98.3%;
Conservative
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M., Mathiesen M.J.,
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18938 MW;
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18818 MW;
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Pred. No. 1.1e-31;
1; Mismatches 2;
                                                                                                         Score 739; DB 2;
Pred. No. 8.4e-28;
5; Mismatches 13
                                                                                                                                                        79B435D0B37DA36D CRC64;
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031115;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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Q44705;
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EMBL; U01892; AAA16057.1; -.
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 212 AA; 22270 MW; FB2E
         Wang I. N., Dykhuizen D.E., Dunn J.
Submitted (OCT-1997) to the EMBL/Ge
EMBL, AF029862; AAB86545.1; -.
InterPro; IPR001800; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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                                                                                            Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                                                                                                  Borrelia burgdorferi (Lyme
                                                                                                                                    OUTER SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                           139;
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1 (TrEMBLrel.
1CE PROTEIN C
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Sampieri A., Dias F.,
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Lipoprotein_6; 1.
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spirochaetaceae;
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Last annotation updat
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Last
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EMBL/GenBank/DDBJ
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Pred. No. 9.5e
21; Mismatches
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                                                                                                                   spirochete).
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FB2EF2673A384276
                                                                                                      Szczepanski A.,
pression of p23
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                                .5e-24;
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                                                                                                                                       ery Match 35.9%;
Sest Local Similarity 70.7%;
Matches 133; Conservative 23
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SEQUENCE
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN C (FRAGMENT).
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                                                                                                                                                                                                                                                                                               Borrelia tanukii.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=56146;
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191 KELTSPVV 198
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193 AA;
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20596 MW; 018A4CB310475A58 CRC64;
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22; Mismatches
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Search completed: March 18, 2002, 10:10:55 Job time: 978 sec

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ALIGNMENTS

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RESULT AAB62724 PTTTXRACTOR POTTT H Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses Chimeric -Chimeric -03-APR-2001 (first entry) WPI; 2001-050113/06. N-PSDB; AAF29028. Borrelia; ospC; Lyme disease; vaccine; chimeric protein; tick Borrelia sp chimeric ospC protein SEQ ID AAB62724; AAB62724 standard; to Lyme disease Dattwyler RJ, (UYNY) UNIV NEW YORK STATE RES FOUND. (BROO-) BROOK BIOTECHNOLOGIES INC. 18-JUN-1999; 19-JUN-2000; 2000WO-US16915 28-DEC-2000 WO200078966-A1 Borrelia Borrelia Seinost G, 9905-0140042 Protein; sp. Dykhuizen D, 560 ₹ Luft ŏ: 52 밍 Gomes-Solecki

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95.1%;
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to immunize
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Pred. No. 1.8e-109;
0; Mismatches 7;
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detect immune
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These may be
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Matches 364; Conserv
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        AAB62726
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DB; AAF29031.
        standard;
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Borrelia
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       Protein;
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Pred. No. 3e-109;
0; Mismatches 4;
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Matches 374
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Lyme disease are used
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)B; AAF29030.
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Borrelia
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Pred. No. 1.3e-107;
1; Mismatches 3;
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Chimeric -
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Lyme disease are used
to Lyme disease -
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                                                                                                                                                                                                                                        Claim 43; Page 147-148; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB62737;
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Borrelia sp.
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66.7%;
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                                                                                                      Score 1726.5; DB 22
Pred. No. 2.2e-107;
2; Mismatches 3;
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                                    Claim 43;
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DB; AAF29015.
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                                    Page 81; 160pp; English
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Borrelia
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The present invention provides compositions comprising ospC proteins and chimeric ospC proteins from members of the Borrelia genus. These may be Borrelia burgdorferi, B. afzelii or B. garinii. These can be used as vaccines against Borrelia infection, which is spread by ticks and leads

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Query Match Best Local Matches

al Similarity 309; Conserv

Conservative

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Mismatches

Indels

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Gaps

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Length 373;

54.2%;

Score 1491.5; Pred. No. 9.3

3e-92 DB 22; 43;

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            Compositions of OspC polypeptides Lyme disease are used to immunize
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                                                                                                                                                                                     Borrelia sp chimeric ospC protein SEQ ID NO:
                                                                                                                                                                                                                                 AAB62729 standard; Protein;
      to Lyme
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Matches 308; Conser
WPI; 2001-050113/06
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Chimeric - Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia sp chimeric ospC protein SEQ
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                                                                                             (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions of OspC polypeptides from strains of Borrelia which cause Lyme disease are used to immunize animals and detect immune responses to Lyme disease .
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Lyme disease are used
to Lyme disease -
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Borrelia
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 Borrelia;
                Borrelia sp chimeric ospC
                                  03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                            to Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                    vaccines against Borrelia infection, which is spread by
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ospC; Lyme disease;
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Lyme disease are used
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N-PSDB; AAF29042.
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Pred. No. 4.1e-89;
9; Mismatches 31
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             vaccines against Borrelia infection, which is spread by ticks to Lyme disease.
                            chimeric ospC proteins from members of the Borrelia genus. These Borrelia burgdorferi, B. afzelii or B. garinii. These can be used
                                                                       Sequence
                                                         Claim 43; Page 136-137; 160pp;
                                                                                                     WPI; 2001-050113/06.
N-PSDB; AAF29037.
                                                                                                                           Dattwyler
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                                           The present invention provides compositions comprising ospC proteins
                                                                                                                                        (UYNY ) UNIV NEW YORK STATE RES FOUND (BROO-) BROOK BIOTECHNOLOGIES INC.
                                                                                                                                                              18-JUN-1999;
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Query Match Best Local

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Search completed: March 18, 2002, 09:54:35 Job time: 333 sec

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Maximum Match 100%
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ALIGNMENTS

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US-09-596-746-52
Sequence 52, Application US/09596746
GENERAL INFORMATION:
APPLICANT: Bettwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
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                                                                                                                                                                    ; TYPE: PRT; ORGANISM: OSPC Chimera US-09-596-746-52
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SEQ ID NO 52
LENGTH: 560
                                                                         Query Match
Best Local Similarity
Matches 560; Conserv
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CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D.
FILE REFERENCE: 2631,1002-001
FastSEQ
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                                                                                          100.0%; Score 2750; DB 19; 100.0%; Pred. No. 1.1e-180;
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                                                                                                                                                                                                  APPLICANT: Dykhuizen, Danial APPLICANT: Luft, Benjamin J. APPLICANT: Luft, Benjamin J. APPLICANT: Maria J.C. Gomes-Solecki ITLE OF INVENTION: Groups of Borrelia burgdorferi and ITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humans FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
RUMBER OF SED ID NOS: 84
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                                                                                                                                                                                                                                                                                                                                                     Application US/09596746A
                                                                                                                                                                                                                                                                                                                                  Dattwyler, Raymond J.
                                                                                                                                                                                                                                                                                                                      Seinost, Gerald
                                                                                                    Length 560;
                                                                                Indels
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                                                                              Gaps
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APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzeili That Cause Lyme Disea
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT APPLICATION NUMBER: US/09/596,746
PRIOR APPLICATION NUMBER: 050/140,042
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Best Local Similarity 95.1
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; GENERAL INFORMATION:
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SEQ ID NO 84
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                                                                                                                                                                                                                                                         LENGTH: 410
TYPE: PRT
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SEEFTNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVA 367
                                             LAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKC 307
                                                                                     AESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDE 247
                              LAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKC
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FastSEQ for Windows Version 4.0
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95.1%;
                                                                                                                                                              Score 1758; DB 19;
Pred. No. 1.6e-112;
                                                                                                                                                  Mismatches
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                                                                                                                                                                           Length 410;
                                                                                                                                                  Indels
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US-09-596-746A-84
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Best Local Sim
Matches 366;
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SEQ ID NO 84
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEO ID NOS: 84
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TYPE: PRT
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VKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEE
                           LKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKS 535
                                                              VKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEE
                                                                                                              LTNSVKELGH------RNNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLA 415
                                                                                                                                                               SEEFTNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVA 367
                                                                                                                                                                                                                 LAKKAIGOKIDNNNGLAALNNONGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKC
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              LKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKS
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FastSEQ for Windows Version
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Seinost, Gerald
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                  63.9%; Score 1758; DB 19; 95.1%; Pred. No. 1.6e-112; tive 0; Mismatches 7;
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US-09-596-746A-58

Sequence 58, Application US/09596746A

GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes Solecki
TITLE OF INVENTION: Groups of Borrelia
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; ORGANISM: OSPC
US-09-596-746-58
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SOFTWARE: FastSEQ for
SEQ ID NO 58
LENGTH: 386
TYPE: PRT
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; GENERAL INFORMATION:
; APPLICANT: Dattwyle
; APPLICANT: Seinost,
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Best Local Similarity
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APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
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361
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            KAAQAALTNSVKELTNPVVA 560
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95.8%;
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Pred. No. 2.8e
0; Mismatches
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2.8e-112;
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Luft, Benjamin J.
Maria J.C. Gomes-Solecki
VENTION: Groups of Borre

Borrelia

burgdorferi

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FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 385
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US-09-596-746A-58
                                                                                                                                                                                                                                                                                                          Sequence 56, Application US/09596746A GENERAL INFORMATION:
LENGTH: 385
TYPE: PRT
ORGANISM: ospC Chimera
-09-596-746A-56
                                                                                                                                                                   APPLICANT: Luft, Benjamin J.
APPLICANY: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
FILE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                     APPLICANT: Dattwyler, Raymond J. APPLICANT: Seinost, Gerald APPLICANT: Dykhuizen, Danial
                                                                                                                                                                                                                                                                                                                                          -09-596-746A-56
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Best Local Similarity 95.8%;
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SEQ ID NO 58
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CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILLING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEO ID NOS: 84
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Pred. No. 2.8e-112;
0; Mismatches 4;
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Query Match
Best Local Similarity
Matches 374; Conserv

Conservative

62.9%;

Score 1729.5; Pred. No. 1.3e 1; Mismatches

1.3e-110; hes 3;

DB 19;

Length 384;

181;

Gaps

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; TYPE: PRT; ORGANISM: OSPC Chimera US-09-596-746-56
                                    SOFTWARE: Fas
SOFTWARE: Fas
SEQ ID NO 56
FRIGTH: 384
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US-09-596-746-56
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APPLICANT: Seinost, Gerald
APPLICANT: Dykhnizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
                                                  NUMBER OF SEQ ID NOS: 84
NUMBER OF SEG ID NOS: 84
PastsEQ for Windows Version
                                                                                        CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILLING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
                                                                                                                                          TITLE OF INVENTION: Groups of Borrelia burilitie OF INVENTION: Borrelia afzelii That FILE REFERENCE: 2631.1002-001
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Best Local Similarity
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Pred. No. 6.1
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APPLICANT: Luft, Benjamin J.

APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease in Humerite Cof Invention: Borrelia afzelii That Cause Lyme Disease in Humerite Reference: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 408
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-596-746-78
; Sequence 78, Application US/09596746
; GENERAL INFORMATION:
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US-09-596-746-78
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|-----KKPFHGNNSGGDSASTNPDESAKGPNLTVISKKITDSNAFILAVKEVEA 239
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                                                1 Similarity
373; Conserv
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Dykhuizen, Danial
                                                                                                                                                                                                                                                                                                                                                                                                         Dattwyler,
                                                Conservative
                                                             62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                           Raymond J.
                                             Score 1726.5; DB 19; Length 408; Pred. No. 2.4e-110; Mismatches 3; Indels 181;
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                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042 PRIOR FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 78, Application US/09596746A GENERAL INFORMATION:
                                                                                          Matches
                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dattwyler, Raymond J.
APPLICANT: Seinost, Gerald
APPLICANT: Dykhuizen, Danial
APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                 LENGTH: 40
TYPE: PRT
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                                                                                          Local Similarity 66.7 hes 373; Conservative
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                              EAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGAKELEELFKSLESLSK
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GKKIHONNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNK 121
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                                                                                                       62.8%;
66.7%;
                                                                                         Score 1726.5; DB 19
Pred. No. 2.4e-110;
2; Mismatches 3;
                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                       Lyme Disease in Humans
                                                                                          Indels 181;
                                                                                                                        Length
                                                                                          Gaps
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APPLICANT: Seinost,
APPLICANT: Seinost,
APPLICANT: Dykhuize,
APPLICANT: Luft, Be
APPLICANT: Maria J.
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                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             SOFTWARE: 1
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26,
4.
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disease ILE REFERIOE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                 LENGTH:
                                  61
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              IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
                                                                      MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                          MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
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                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version
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Maria J.C. Gomes-Solecki
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                                                                                                                      Conservative
                                                                                                                 54.4%; Score 1496.5; DB
82.7%; Pred. No. 1.5e-94;
tive 21; Mismatches 43
                                                                                                                                               DB 19; Length
                                                                                                                    43;
                                                                                                                    Indels
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SEQ ID NO 24
LENGTH: 375
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme Di FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746A
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/140,042
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OTHER INFORMATION: OspC Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
 240
                               241 LVLSIDELAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTE
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                                                                                                                                                                                                                                                                                                     MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                      ELTSPVVAESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVET
                                                                                                                                                         KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                                  MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
LLTSIDELA-KAIGKKIKNDVSLDNEADHNGSLISGAYLISNLITKKISAIKDSGELKAE
                                                                                                                                         KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
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Maria J.C. Gomes-Solecki
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                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-06-18
                                                                                                                                                                                                                                                                                                                                                  54.3%; Score 1492; DB 19;
83.5%; Pred. No. 3e-94;
tive 20; Mismatches 40;
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APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
ITLE OF INVENTION: Borrelia afzelii That Cause Lyme Disea
ILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 26
SEQ ID NO 26
SEQ ID NO 27
COGANISM: Artificial Sequence
FEATURE:
RESULT 14
US-09-596-746-62
; Sequence 62, Application US/09596746
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US-09-596-746-26
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GENERAL INFORMATION:
APPLICANT: Dattwyler, Raymond J.
APPLICANT: Scinost, Gerald
APPLICANT: Dykhuizen, Danial
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKAAQVALTNSVKEL 375
                                                                                                         KAAQVALTNSVKEL 375
                                                                                                                                                        ENAKKCSEDFTKKLEGEHAQLGIENVTDENAKKAILITDAAKDKGAAELEKLFKAVENLA 359
                                                                                                                                                                                                                       LKEKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE 181
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                                                                                                                                                                                        AKAKKCSEEFTNKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLL 361
                                                                                                                                                                                                                                                                                                                                                                 LKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKE 180
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                                                                                         KAAKEMLANSVKEL 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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FILE REFERENCE: 2631.1002-001
CURRENT APPLICATION NUMBER: US/09/596,746
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/140,042
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 397
TYPE: PAT
ORGANISM: OSPC Chimera
US-09-596-746-62
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                                                                                                                                                                                                                                     Sequence 62, Application US/09596746A
GENERAL INFORMATION:
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                                                                                                APPLICANT: Luft, Benjamin J.
APPLICANT: Maria J.C. Gomes-Solecki
TITLE OF INVENTION: Groups of Borrelia burgdorferi and
TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D:
FILE REFERENCE: 2631.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Groups of Borrelia burgdorferi and TITLE OF INVENTION: Borrelia afzelii That Cause Lyme D
                                             CURRENT APPLICATION NUMBER: US/09/596,746A CURRENT FILING DATE: 2000-06-19 PRIOR APPLICATION NUMBER: US 60/140,042
                                                                                                                                                                                     APPLICANT:
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                             PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
                 NUMBER OF SEQ ID NOS:
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: Dykhuizen, Danial
: Luft, Benjamin J.
: Maria J.C. Gomes-Sol
FastSEQ for Windows Version 4.0
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Seinost, Gerald
                               1999-06-18
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                                                                                                                                                                                                                         ; SEQ ID NO 62
; LENGTH: 398
; TYPE: PRT
; ORGANISM: OSPC Chimera
US-09-596-746A-62
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362 KAAQVALTNSVKEL 375
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385 KAAKEMLANSVKEL 398
                        1; Gaps
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Search completed: March 18, 2002, 10:08:47 Job time: 975 sec

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Title:
Perfect score:
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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1 MACNNSGKDGNTSANS
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US-09-126-293-15
US-08-128-353-3
US-08-235-836C-107
US-08-235-836C-34
US-08-235-836C-34
US-08-235-836C-34
US-08-235-836C-34
US-08-235-836C-36
US-09-196-293-11
US-08-128-353-2
US-08-128-353-2
US-08-128-353-2
US-08-128-353-2
US-08-235-836C-32
US-08-933-462-9
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US-08-933-462-9
US-08-933-992A-6
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Sequence 110, App
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Sequence 10, Appli
Sequence 110, Appli
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Query Match 35.9%; Score 986.5; DB 4; Best Local Similarity 51.1%; Pred. No. 8e-63; Matches 256; Conservative 42; Mismatches 132;

Length Indels

466; 71;

Gaps

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1 MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60

LASSIFICATION: 435 OR APPLICATION DATA: PPLICATION NUMBER: ILING DATE: 01-11-9 ORNEY/AGENT INFORMAT AME: BOGOSIAN MAFE: EFERENCE/DOCKET NUMBER: EFEREN	RESULT 1 US-08-235-836C-110 US-08-235-836C-110 US-08-235-836C-110 Sequence 110, Application US/08235836C Patent No. 6248562 Fatent No. 6248562 Fatent No. 6248562 Fatent No. 6248562 Fatent No. 6248562el Chimeric Proteins TITLE OF INVENTION: No. 6248562el Chimeric Proteins TITLE OF INVENTION: No. 6248562el Chimeric Proteins NUMBER OF SEQUENCES: 144 CORRESPONDENCE ADDRESS: ADDRESSEE: Brookhaven National Laboratory STREET: CITY: Upton STATE: NY COUNTRY: USA ZIP: 11973 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: DATA: APPLICATION NUMBER: US/08/235,836C FILING DATE: 29-APR-1994 FULING DATE: 29-APR-1994	28 177.5 6.5 1196 2 US-08-735-893-4 29 177 6.4 3248 1 US-08-655-776-1 30 176.5 6.4 3248 1 US-08-655-776-1 31 176.5 6.4 3248 5 PCT-US95-16216-1 32 175.5 6.4 3248 5 PCT-US95-16216-1 33 174 6.3 748 1 US-08-328-254-6 34 173 6.3 1038 4 US-09-541-782-4 35 171 6.2 1104 4 US-09-541-782-4 36 170.5 6.2 1151 3 US-08-840-006-5 39 170.5 6.2 1151 3 US-08-840-006-5 39 170.5 6.2 3111 2 US-08-460-309-4 40 170.5 6.2 3111 2 US-08-460-309-4 41 167 6.1 1147 3 US-08-470-260-5 42 167 6.1 1147 3 US-08-471-491-5 43 167 6.1 1147 4 US-08-195-487-4 45 167 6.1 2101 5 PCT-US93-06160-4 ALIGNMENTS
	Uses Therefor	Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli

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RESULT 2
US-08-235-836C-30
; Sequence 30, Application US/08235836C
; Patent No. 6248562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent NO. 0270...
GENERAL INFORMATION:
APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: APPLICANT: No. 6248562el Chimeric Proteins Comprising
                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                               REFERENCE/DOCKET NUMBER: BN
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                          TELEPHONE:
                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0:
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
                                                                                                               NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 KDLFES--VEGLIKAAQVALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTVISKKITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Upton
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 GKTLVSKKVTSKDKSSTEEKFNEKGEVSEKIITRADGTR-----LEYTGIKSDGSGKA
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ZIP: 11973
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                                                             (516) 282-7338
                                                                                                                                                                                                                                                                        us/08/235,836C
                                                                                                   BNL93-28A
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APPLICANT: Soutscheck, Erwin
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac Mursic, Vora
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorferi
FILE REFERENCE: 738.001US2
CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1992-06-19
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
EARLIER APPLICATION NUMBER: WO PCT/EP90/02282
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; ORGANISM: Borrelia burgdorferi
US-09-196-293-15
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 15
LENGTH: 209
                                                                                                                                                  Matches
                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                  LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: DE P40 18 988.0 EARLIER FILING DATE: 1990-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: DE P39 42 728.5 EARLIER FILING DATE: 1989-12-22
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61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
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TYPE: amino acid
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Local Similarity 98.4%;
                                                          MACNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA
                                                                                                                                                188;
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                                                                                                                                                Conservative
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                                                                                                                                                              33.7%;
                                                                                                                                                              Score 928; DB 4
Pred. No. 4e-59;
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Pred. No. 2.1e-59;
                                                                                                                                            Mismatches
                                                                                                                                                                              DB 4; Length 209
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Best Local Similarity
Matches 188; Conserv
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MOLECULE TYPE:
08-158-353-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acidi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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   197
                                                           181 ELTSPVVAESP 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                            ELTSPVVAESP 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                         KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08158353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 928; DB 1
Pred. No. 4e-59;
2; Mismatches
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US-08-235-836C-122
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Patent No.
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Best Local S
Matches 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (516) 282-37
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, MATGARET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Dunn, John J.
APPLICANT: Dunn, J.
APPLICANT:
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FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                     466
                                                                                                                                            406
                                                                                                                                                                                                              124
                                                                  184 SPVVAESPAMGSNSGKGGDSASTN 207
                                                                                                                                                                                                                                                                                346 KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 405
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STATE: NY
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                                                                                                                                                                                                                                                                                                                 64 KIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
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SPVVAESPK-----KPGTMAQYN
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                                                                                                                                            EKHTDLGKEGVTDADAKEA I LKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT
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5. 6248562
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Pred. No. 4.3e-58;
Pred. No. 4.3e-58;
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US-08-209-603E-15; Sequence 15; Application; Patent No. 6248538; GENERAL INFORMATION:

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REFERENCE/DOCKET NUMBER: 27.224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 597-3355
TELEPAX: (212) 597-3355
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 210
TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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ANTI-SENSE: N/A
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: DSM 5
 181 ELTSPVVAESP 191
                           137 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 0
FILING DATE: 19-JUN-1992
                                               121 KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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                                                                                                                  61 IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETETN 120
                                                                                                           77
                                                                                                                                                                   17 ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVLEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION:
                                                                                                                                                                                      APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 136
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99 PARK AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOTZ, MANFRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                              33.5%;
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                                                                                                                                                                                                                                                                                                                                                  amino acid analysis
                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                         Score 921; DB 4;
Pred. No. 1.3e-58;
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US-08-235-836C-34; Sequence 34, Application US/08235836C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08,
APPLICATION NUMBER: US 08,
FILING DATE: 01-11-93
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING CONTROL OF THE PROPERTY APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/235,836C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dunn, John J.
APPLICANT: Luft, Benjamin J.
APPLICANT: Luft, Benjamin J.
TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 282-7338
                                                                                                                                                                396
                                                                                             456
                                                                                                                            184 SPVVAESP 191
                                                                                                                                                                         124 EKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT 183
                                                                                                                                                                                                                                  336
                                                                                                                                                                                                                                                                                          STATE: NV
                                                                                                                                                                                                                                           64 KIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 29-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                        AKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT
                                                                                                                                                                                                                       KIHQNNGLDTEYNHNGSLLAGRYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLK 395
                                                                                           SPVVAESP
                                                                                                                                                                                                                                                                                                                                                                      186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 amino acids
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
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V: 435
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                                                                                                                                                                                                                                                                                                                                                                                Score 915; DB 4; Length 466; Pred. No. 1e-57;
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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INFORMATION:

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US-08-158-353-4
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                                                                                                         Sequence 4, Application US/08158353 Patent No. 5620862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 187; Conserv
                                GENERAL INFORMATION:
APPLICANT: Padull, Steven J.
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/148
FILING DATE: 01-11-93
ATTORNEY_AGENT INFORMATION:
NAME: BOGOSIAN, MATGAREC C.
REGISTRATION NUMBER: 25.324
REFERENCE/DOCKET NUMBER: 30.4
REFERENCE/DOCKET NUMBER: DISTRIBUTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (516) 282-3729 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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APPLICANT: Luft, Benjamin J.

TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising

TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
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PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES: 7
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                    LGHRNNSGGDSASTNP--DESAKGP 397
                                                                                                                                                                                                                                                                                                            LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 374
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IBM PC compatible
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                                                                                                                                                                                                                   TSPVVAESPKKP 212
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                                                   Methods for Diagnosing
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Pred. No. 2.4e-56;
1; Mismatches 3;
                                                    Early Lyme
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Best Local S
Matches 186
                                                                                                                                                                                                                                   Patent No. 6248562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                       Sequence 36, Application US/08235836C Patent No. 6248562
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TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,353
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 212 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     APPLICANT: Dunn, John J. APPLICANT: Luft, Benjamin
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                                                                                                                                             CORRESPONDENCE ADDRESS
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STATE:
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                                              COUNTRY: USA
ZIP: 11973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: Two Militia Drive
                                                                                             CITY: Upton
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                                                                              STATE:
                                                                                                             STREET:
                                                                                                                          ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                  LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 314
                                                                                                                                                                                                                                                                                                                                                                                                                 LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
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                                                                                                                                                                       No. 6248562el Chimeric Proteins Comprising
Borrelia Polypeptides and Uses Therefor
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90.7%;
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Pred. No. 4e-56;
2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/196,293
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: US 08/209,603
EARLIER FILING DATE: 1994-03-10
EARLIER FILING DATE: 1994-03-10
EARLIER APPLICATION NUMBER: US 07/862,535
EARLIER FILING DATE: 1992-06-19
EARLIER FILING DATE: 1990-12-21
EARLIER FILING DATE: 1990-12-21
EARLIER APPLICATION NUMBER: DE P39 42 728.5
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER APPLICATION NUMBER: DE P40 18 988.0
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                           APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Motz, Manfred
APPLICANT: Soutscheck, Erwin
APPLICANT: Wilske, Bettina
APPLICANT: Preac-Mursic, Vera
TITLE OF INVENTION: Active proteins from Borrelia
TITLE OF INVENTION: burgdorfer1
TILE REFERENCE: 738,001US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local 9
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TELEFAX: (516) 282-3729
INFORMATION FOR SEQ ID NO: 36
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ATTORNEY/AGENT INFORMATION:
NAME: BOGOSÍAN, MATGATET C.
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: BNL9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -196-293-11
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LENGTH: 207 amino acid:
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSBELKKKIKEAKDCSQKFTTKLKDSH 498
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hes 181; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIK 79
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PatentIn Release #1.0, Version #1.25
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Windows Version 4.0
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 882; DB 4; Length 207; Pred. No. 7.4e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP90/(
APPLICATION NUMBER: PCT/EP90/(
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862
FILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION:

NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: LKR-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08209603E Patent No. 6248538
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Best Local Similarity
Matches 182; Conserv
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LENGTH: 212
                                                TELEFAX: (212) 557-56
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         COMPUTER: AT&T - IBM COMPATIBLE OPERATING SYSTEM: MS-DOS Version SOFTWARE: ASCII CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" FLOPPY DISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNOLOGICALITY OF INVENTION: FROM BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
LENGTH:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/209,603E FILING DATE: 10-MAR-1994 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 LGHRNNSGGDSASTNP--DESAKGP 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 LKSGHADLGKODATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 314
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U:
ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BROOK AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREAC-MURSIC, MOTZ, MANFRED
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                                           2) v.,
, 557-5635
, no: 11:
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Pred. No. 3.9e-54;
2; Mismatches 7;
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MOLECULE TYPE:

TOPOLOGY: LINEAR

DESCRIPTION: PROTEIN

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                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08158353
Patent No. 5620862
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Padula, Steven J.
TITLE OF INVENTION: Methods for
TITLE OF INVENTION: Disease
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAITO11, Alice O.
REGISTRATION NUMBER: 3,542
REFERENCE/DOCKET NUMBER: UCT9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
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st Local Similarity 88.8%;
tches 182; Conservat****
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
PUBLICATION INFORMATION:
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: B. BURGDORFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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LIBRARY: DSM 5662
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                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                            ZIP: 02173
                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                         Lexington
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                                                                                                                                                                                                                                                                                                           E: Hamilton, Brook, Smith & Reynolds, P. Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                       Padula, Steven J.

VENTION: Methods for Diagnosing Early Lyme

VENTION: Disease
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                                                                                                                                                                                                                                                            USA
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                                    UCT93-05
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Pred. No. 3.9e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
APPLICATION NUMBER: US 07/727,245
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/142:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                          FILING DATE: 25-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            FILING DATE: 1993031:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AN
TITLE OF INVENTION: PREVENTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "'
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                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                           20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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25-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHOD AND COMPOSITION FOR THE PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 676; DB 1; 74.7%; Pred. No. 3.7e-41;
                                                                                                                                                                               US 07/824,161
                                                                                                                                                                                                                                                                                              US/08/031,295
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                                                  30472/142 IMMU
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: AMINO ACID

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RESULT 15
US-07-903-580-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07903580
Patent No. 6221363
GENERAL INFORMATION:
APPLICANT: LIVEY, Ian
APPLICANT: DORNER, Freidrich
TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE
TITLE OF INVENTION: PREVENTION OF LYME DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 142;
               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,580
                                                                           REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                   APPLICATION NUMBER: US 07/824,161
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/727,245
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 VKELTSPVVAESP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1800 Diag
CITY: Alexandria
STATE: Virginia
                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
LENGTH:
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: UPFILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 ISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVSSIDELATK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MACNNSGKDGNT-SANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAK 59 ::||||||| |::|||||:||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                            899149
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                                                                                                                                            30472/131 IMMU
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                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-07-903-580-2
                                                                                                                                                                                                                                                   Query Match 24.0%;
Best Local Similarity 73.6%;
Matches 142; Conservative 1
              179 VKELTSPVVAESP 191
                                                              137
                                                                             119 TNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANS 178
                                                                                                                             77
                                                                                                                                                                                     60 AIGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEG-LKEKIDAAKKCSETF 118
                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID TOPOLOGY: linear
VKELTSPVVAETP 209
                                                             TKKLAAGHAQLGIDGATDNDSKEAILKTNGTKTKGAEELVKLSESVASLSKAAQEASANS 196
                                                                                                                          AIGKKIQQNNGLGANADKNGSLLAGAYAISTLITEKLKALKNSGELKAKIEDAKKCSEDF 136
                                                                                                                                                                                                                                                   ; Score 661; DB 4; I; Pred. No. 4.4e-40; 14; Mismatches 35;
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Search completed: March 18, 2002, 09:55:36 Job time: 349 sec

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Run

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1 MACNITT
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      BLOSUM62
Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
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/cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
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US-09-748-875-61
US-09-748-875-61
US-09-748-875-62
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US-09-708-427-15046
US-10-072-851-155046
US-09-708-427-15044
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US-09-815-242-13080
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            Sequence 7, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 60, Appli
Sequence 14, Appli
Sequence 61, Appli
Sequence 61, Appli
Sequence 63, Appli
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Sequence 7646, A
Sequence 1590, A
Sequence 15046, A
Sequence 15046, A
Sequence 15044, A
Sequence 10224, A
Sequence 10311, Ap
Sequence 10311, Ap
Sequence 3730, Ap
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US-09-974-992-7
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1	1725	5795	5795	2434	2434	3158	3158	1786	1489	837	837	576775	576775	576775	730	1018	1014	2344	2344	2056
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02 10 031 102 12	115-10-037-183-13	US-10-072-851-12610	US-09-815-242-12610	US-10-072-851-5835	US-09-815-242-5835	US-10-072-851-12611	US-09-815-242-12611	US-09-742-096-3	US-09-614-150-6636	US-10-072-851-5883	US-09-815-242-5883	US-09-895-611D-2	US-08-895-611D-2	US-08-895-611-2	US-09-708-427-3731	US-09-708-427-19882	US-09-708-427-19883	US-10-072-851-12713	US-09-815-242-12713	US-09-614-150-4824
seduence is, obbi	3	Sequence 12610, A	Sequence 12610, A	Sequence 5835, Ap	Sequence 5835, Ap	Sequence 12611, A	Sequence 12611, A	Sequence 3, Appli	Sequence 6636, Ap	Sequence 5883, Ap	38	Sequence 2, Appli		Sequence 2, Appli	Sequence 3731, Ap	Sequence 19882, A	Sequence 19883, A	Sequence 12713, A	Sequence 12713, A	Sequence 4824, Ap

ALIGNMENTS

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; ORGANISM: Borrelia afzelii
US-09-974-992-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Query Match 32.2%;
Best Local Similarity 90.7%;
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mathiesen, Marianne J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 212
TYPE: PRT
                                                                                                                                                                                                                                         375 LGHRNNSGGDSASTNP--DESAKGP 397
                                                                                                                                                         LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 374
                                                                              LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
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-TSPVVAESPKKP 212
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Pred. No. 7.9e-49;
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Gaps

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CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DX97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 211
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TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-6666p
CURRENT APPLICATION NUMBER: US/09/974,992
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR APPLICATION NUMBER: 09/180,089
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: PCT/DK97/00203
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEO ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
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       Matches 148;
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.9%;
Best Local Similarity 98.9%;
                                                                                                                                                                                                                                                                                                                    APPLICANT: Mathlesen, Marianne J.,
APPLICANT: Theisen, Michael
APPLICANT: Holm, Arne
APPLICANT: Ostergaard, Soren
TITLE OF INVENTION: Novel OspC-derived peptide fragments
FILE REFERENCE: 459-666P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Applicat GENERAL INFORMATION:
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                                                                                                            ORGANISM: Borrelia burgdorferi
                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  uence 5, Application US/09974992
NERAL INFORMATION:
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       Conservative
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 24.5%; Score 674.5; DB 6
76.7%; Pred. No. 1.6e-35;
ative 11; Mismatches 31
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Pred. No. 2.4e-48;
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                                    6;
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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-748-875-1
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US-09-748-875-1
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TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT FILING DATE: 2000-12-26
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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         443
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VKEEANESRNEEKIKQAKEKVES--KKAEATRLEKIKT---DRKKAEEEAKRKAEESEK-
                                    LKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKELGHRNNSGGDSASTNPDESAKG 396
                                                                                                                ----KTEIAKAKKCSEEF--
                                                                                                                                                                                        DNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLK---NLEEL-------
                                                                         DTLKPEKKVAEAEKKVEEAKKKAKDQKEEDRRNYPTNTYKTLELEIAESDVKVKEAELEL
                                                                                                                                                   DRRK-----HTQNVNLNIKLSAIKTKYLYELSVLKENSKKEELTSKTKAELTAAFEQFKK 382
                                                                                                                                                                                                                                                                                                  KIKQAEAEVESKQAEATRLKKIKTDREEAKRKADAKLKEAVEKNVATSEQDKPKRRAKRG
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                                                                                                                                                                                                                                                                                                                                                                                                               AKKCSETFTNKLKEKHTD------LGKE-GVTDADAKEAILKTNGTKTKGAEELG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LITKLSEIKKKYLYDLKVNVLSEAELTSKTKETKEKLTATFEQFKKDTLPTEPEKKVAEA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGVRSGNNLTVTSSGQDISKKYAD-----EVESHLESILKDVKKNLKKVQHTQNVG 88
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; Pred. No. 4.2e-07;
94; Mismatches 260; Indels 132;
                                                                                                              -TNKLKSGHADLGKQDATDDHAKAAI 336
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RESULT 5
US-09-748-875-60
; Sequence 60, Application US/09748875
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
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CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 60
LENGTH: 929
TYPE: PRT
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US-09-748-875-60
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Best Local S
Matches 144
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                                                                                                                                                                                                                                                                                                                                                                                                                           111
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nes 144; Conserv
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PNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAG : |: | : | | | | | | |
                                                   VKEEANESRNEEKIKQAKEKVES--KKAEATRLEKIKT---DRKKAEEEAKRKAEESEK-
                                                                                                                    DTLKPEKKVAEAEKKVEEAKKKAKDQKEEDRRNYPTNTYKTLELEIAESDVKVKEAELEL
                                                                                                                                                    ----KTEIAKAKKCSEEF------TNKLKSGHADLGKQDATDDHAKAAI
                                                                                                                                                                                     DRRK-----HTQNVNLNIKLSAIKTKYLYELSVLKENSKKEELTSKTKAELTAAFEQFKK
                                                                                                                                                                                                                       DNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLK---NLEEL---------
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                                                                                 LKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKELGHRNNSGGDSASTNPDESAKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 234; DB 5;
Pred. No. 6.3e-07;
4; Mismatches 260
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US-09-748-875-2
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Matches 139
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SEQ ID NO 2
LENGTH: 707
TYPE: PRT
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APPLICANT: BRILES et al.

TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),

TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR

FILE REFERENCE: 454312-3140

CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 2000-12-26

CURRENT FILING DATE: 2000-12-26
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PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
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                                          EAKQKVDAEEYAL----EAKIAELEYEVQRLEKELKEIDESDSEDYLKEGLRAPLQ--S
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22.2%; Pred. No. 7.7e-07;
tive 100; Mismatches 264;
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US-09-748-875-14
Sequence 14, Application US/09748875
GENERAL INFORMATION:
APPLICANT BRILES et al.
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Best Local Similarity
Matches 148; Conser
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PRENT FILING DATE: 2000-12-26
RIOR APPLICATION NUMBER: 09/298,523
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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TYPE: PRT
 513 LQ--SKLDTKKAKLSKLEELSDKIDELDAEIAKLEVQLKDA----
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; Pred. No. 8.1e-07;
89; Mismatches 247; Indels 142; Gaps
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--EGNNVEAYF 561
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; SEQ ID NO 61
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-748-875-61
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APPLICANT: BRILES et al.
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC),
TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
FILE REFERENCE: 454312-3140
CURRENT APPLICATION NUMBER: US/09/748,875
CURRENT FILING DATE: 2000-12-06
CURRENT FILING DATE: 2000-12-06
CURRENT FILING DATE: 2000-12-06
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 OKKVEEAKKKAEDOKEKDRRNYPTITYKTLELEIAESDVEVKKAELELVKVKAKESODEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AKKCSETFTNKLKEKHTD------LGKE-GVTDADAKEAILKTNGTKTKGAEELG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 LDTE-----YNHNGSLLAGAYAIS-----TLIKQKLDGLKNEGLKEKIDA 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 ESVK-GPNLT-----EISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIH-QNNG
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                                     THGTKDKGAKELEELFKSLESLSKAAQAA 546
                                                                         Q--SKLDTKKAKLSKLEELSDKIDELDAEIAKLEVQLKDAEGNNNVEAYFKEGLEKTTAE
KKAELEKAEADLKKAVDEPETPAPAPQPA 636
                                                                                                                                              -KAAEAKQKVDAEEYAL-----EAKIAELEYEVQRLEKELKEIDESDSEDYLKEGLRAPL
                                                                                                                                                                                                                                                                                              DTLKPEKKVAEAEKKVEEAKKKAKDQKEEDRRNYPTNTYKTLELEAESDVKVKEAELELV 442
                                                                                                                                                                                                                                                                                                                                      -----KTEIAKAKKCSEEFTNKLKSGHAD-------LGKQDATDDHAKAAIL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSGELATPDKKENDAKSSD-SSVGEETLPSPSLNMANESQTEHRKDVDEYIKKMLSEIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIGQ-KI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIKQAEAEVESKQAEATRLKKIKTDREEAKRKADAKLKEAVEKNVATSEQDKPKRRAKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLFES-VEVLSK----PAMGSNSG
                                                                                                                                                                                                                                                           KTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKELGHRNNSGGDSASTNPDESAKGP 397
                                                                                                                                                                                                                                                                                                                                                                          DRRK-----HTQNVNLNIKLSAIKTKYLYELSVLKENSKKEELTSKTKAELTAAFEQFKK 382
                                                                                                                                                                                                                                                                                                                                                                                                               DNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLK---NLEEL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGVRSGNNLTVTSSGQDISKKYAD------EVESHLESILKDVKKNLKKVQHTQNVG
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Pred. No. 1.9e-06;
Pred. No. 1.9e-06;
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US-09-748-875-62
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CURRENT APPLICATION UNMEER: US/09/748,875
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 09/298,523
PRIOR PILING DATE: 1999-04-23
NUMBER OF SEO ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 62, Application US/09748875
GENERAL INFORMATION:
APPLICANT: BRILES et al.
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ORGANISM: Streptococcus
-09-748-875-62
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608 KKAELEKAEADLKKAVDEPETPAPAPQPA 636
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                                                                       Q--SKLDTKKAKLSKLEELSDKIDELDAEIAKLEVQLKDAEGNNNVEAYFKEGLEKTTAE
                                                                                                                                                                  NLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIKNDGTLDNEANRNESLIAGA 457
                                                                                                                                                                                                                                                                                                                                                                DRRK-----HTQNVNLNIKLSAIKTKYLYELSVLKENSKKEELTSKTKAELTAAFEQFKK
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                                 THGTKDKGAKELEELFKSLESLSKAAQAA 546
                                                                                                     YEISKLITOKLSVLNSEELKKKIKEAKDCSOKFTTKLKDSHAELGIQSVQDDNAKKAILK
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                                                                                                                                         -KAAEAKQKVDAEEYAL----EAKTAELEYEVQRLEKELKEIDESDSEDYLKEGLRAPL
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RESULT

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US-09-748-875-63; Sequence 63, Application; GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 TSYNKANES-----QTEHRK-----AAKQVDEDIKKMLSEIQEYIKKMLSEIQLDKRKH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 TSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIG-----KKIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNN------GLDTEYNHNGSLL---AGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCS 115
                                                                                                                                                                                                                                                                                                           TNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIKNDGTLDNEA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLITEKLSK-----LKNLEELKTEIAKAKKCSEEF----TNKLKSGHADLGKQDA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ELTSPVVAESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKE 237
                                                                                                                   KEGLEKTTAEKKAELEKAEADLKKAVDEPETPAPAPQPA 646
                                                                                                                                                      DDNAKKAILKTHGTKDKGAKELEELFKSLESLSKAAQAA 546
                                                                                                                                                                                              YLKEGLRAPLQ--SKLDTKKAKLSKLEELSDKIDELDAEIAKLEVQLKDAEGNNNVEAYF 607
                                                                                                                                                                                                                                  NRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQ
                                                                                                                                                                                                                                                                       RKAEESEK---KAAEAKQKVDAEEYAL----EAKIAELEYEVQRLEKELKEIDESDSED
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US-09-708-427-19881

Sequence 19881, Application US/09708427

Sequence 19881, Application US/09708427

SERBAL INFORMATION:

ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY
                                                                                                                   RESULT 12
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LENGTH: 670
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CURRENT APPLICATION NUMBER: US/09/748,875

CURRENT FILING DATE: 2000-12-26

PRIOR APPLICATION NUMBER: 09/298,523

PRIOR FILING DATE: 1999-04-23
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SOFTWARE: PatentIn Ver. 2.1
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1269
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..1269
; OTHER INFORMATION: Ceres Seq. ID 1836845
US-09-708-427-19881
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19881
LENGTH: 1269
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Best Local Similarity
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TYPE: PRT
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VNEKLKQEFDQAQEKSLQSSSESELLAETNNQLKIKIQEL
                                                                                             KAMEEFTSRDSEASSLTEKLRDLEGKIKSYEEQLAEASGKSSSLKEKLEQTLGRLAAAES
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                                                                                                                                        KKIK-----EAKDCSQKFTT---KLKDSHAELGIQSVQDDNAKKAILKTHG------
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7646
LENGTH: 1881
TYPE: PRT
ORGANISM: Candida albicans
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GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
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Best Local S
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LOCATION: (1881)..(1881)
OTHER INFORMATION: X-any amino acid
10-032-585-7646
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Local Similarity 21.2%; Pred. No. 4e-05;
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                                                                                                                                           KLSYLNSEELKKKIKEAKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKTHGTKDKGA 526
                                                                                                                                                                                                                                                                                         EKEINDLIRKL-----EAAKSDHDTERKKLSLLIEDTKSESEKNVIKLNEQIEKLKG
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NELTEATSELTKLQDNNQSLTEEIEKTKAALTKSSKDL 1478
                                             KELEELFKSLESLS------KAAQAALTNSVKEL
                                                                                           -----ENLKKEISLLEDQKKDDTTKYKELAAQLETKTSNLDSTTMELEKTELELKKVR
                                                                                                                                                                                           EREKEVRDIQSQLAAKTIDWEKIKTILDKVLKEKS--DLEKTNKESVDTLKKEV-----
                                                                                                                                                                                                                                        -AVKEVEALLSSI------DELSKAIGKKIKNDGTLDNEANRNESLIAGAYEISKLITQ 466
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; LOCATION: (1881)..(1881)
; OTHER INFORMATION: X-any
US-10-072-851-15590
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Best Local Similarity
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TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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TYPE: PRT
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1284 EKEINDLIRKL----
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                                         QVALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTV-ISKKITDSNAFLL-----
                                                                               KSLKHDIEDLKREKIKLE----TTLKENEETMFEKKEQLQVVNDKCKELEACLKKLTETK 1283
                                                                                                              NKLKSGHADLGKQDATDDHAKAAILKTHATTDKGAKE------FKDLFESVEGLLKAA 364
                                                                                                                                                                                                           -IDNNNGLAALNNQNGSLLAGAYAISTLITEKL---SKLKNLEELKTEIAKAKKCSEEFT 312
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                                                                                                                                                                   ESERNDIKSNLDEANKELSDNREKLSNLEKEKTELNNKLKTQEEKISDLETSVAISEDKS
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Ohlsen, Karl L.
Zyskind, Judith W.
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Boone, Charles
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Zamudio, Carlos
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200	Db Oy	Db Qy	Db Qy	, B 8	gb Qy	Db 49	O S	Que Bes Mat	; c 0s-09		~ · · · · ·	SEQ TI	ONEE E	RESULT US-09-	Db	Qy	B .) b	2 29
321 DLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGL 360	268 NQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNKLKSGHA 320	223KKITDSNAFVLAVKEVETLYLSIDELAKKAIGQKIDNNNGLAALN 267 :::	KELTS DSLKS			41HAVKEVEALLSSIDEIAAKAIGKKIHONNG 70	ACNNSG : SCTNSSVEE	Query Match 7.6%; Score 209; DB 6; Length 1144; Best Local Similarity 21.8%; Pred. No. 3.1e-05; Matches 155; Conservative 116; Mismatches 247; Indels 192; Gaps 31;		LOCATION: 1.1144	RE:	CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 EQ ID NO 15046 LENGTH: 1144 TYPE: PAT	N. ALEXANDROV et al. WENTION: SEQUENCE-DETERMINE WENTION: THEREBY INCE: 2750-1243P LICATION WIMBER: 15 /00 /700	15 708-42 ence 1	1441 NELTEATSELTKLQDNNQSLTEEIEKTKAALTKSSKDL 1478	527 KELEELFKSLESLSKAAQAALTNSVKEL 554	1388ENLKKEISLLEDOKKDDTTKYKELAAQLETKTSNLDSTTMELEKTELELKTVR 1440	1336 EREKEVRDIQSQLAAKTTDWEKIKTTLDKVLKEKSDLEKTNKESVDTLKKEV 1387	415

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Search completed: March 18, 2002, 09:58:37 Job time: 395 sec

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Title: Perfect score: Sequence: Searched: Scoring table: Run on: OM protein - protein search, using sw model tal number of hits satisfying chosen parameters: ximum DB seq length: 0 March 18, 2002, 09:56:49; Search time 68.77 Seconds (without alignments) 620.296 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-596-746A-52 2750 1 MACNNSGKDGNTSANSADES......KAAQAALTNSVKELTNPVVA 560 219241 seqs, 76174552 residues GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 219241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SUMMARIES

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674.5 674.5 673.5 672.5	759.5 757.5 756.5 700 696.5 683.5 677.5	928 8921 886 881 878 874 874 834.5 834.5 834.5 831 798	Score
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ALIGNMENTS

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-210 <jau> A;Cross-references: RMBL:X69596; NID:g311391; PIDN:CAAA49306.1; PID:g311392 R;Cross-references: RMBL:X69596; NID:g311391; PIDN:CAAA49306.1; PID:g311392 R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F. Mol. Microbiol. 18, 257-269, 1995 A;Title: Evidence for lateral transfer and recombination in OspC variation in Lyme di A;Title: Evidence for lateral transfer and recombination in OspC variation in Lyme di A;Reference number: S70255; MUID:96296448 A;Recession: S70281 A;Accession: S70281 A;Accession: S70281 A;Accession: S70281 A;Cross-references: Lyme cid sequence not shown A;Molecule type: DNA A;Residues: 19-210 <liv> A;Cross-references: EMBL:L42887; NID:g858715; PIDN:AAB36995.1; PID:g1695212 A;Experimental source: Strain Ip2 C;Genetics: A;Gene: ospC C;Superfamily: Lyme disease spirochete surface protein C</liv></jau>	A;Title: Outer surface protein C gene sequence analysis of Borrelia burgdorferi sensu A;Reference number: I40269; MUID:96025162 A;Accession: I40269; MUID:96025162 A;Accession: I40269 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-210 <res> A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 A;Cross-references: GB:D49497; NID:g707092; PIDN:BAA08457.1; PID:g769684 R;Jauris-Helpke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, E. Med. Microbiol. Immunol. 182, 37-50, 1993 A;Title: Genetic heterogenity of the genes coding for the outer surface protein C (Os A;Reference number: S37726; MUID:93268136 A;Accession: S37726</res>	Nature 390, 580-586, 1997 A;Authors: Smith, H.O.; Venter, J.C. A;Authors: Smith, H.O.; Venter, J.C. A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A;Reference number: A70100; MUID:98065943 A;Accession: G70218 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: BNA A;Residues: 1-210 <kle> A;Cross-references: GB:AE000792; NID:g3253098; PIDN:AAC66329.1; PID:g2689901; TIGR:BB A;Experimental source: strain B31 R;Fukunaga, M.; Hamase, A. T; Ciln Microbiol 33 2415-2420 1995</kle>	RESULT: 1 G70218: G70218: G70218: G70218: G70218: G70218: C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Ju1-2000 C; Date: 13-Feb-1998 #text_change 21-Ju1-2000 C; Date: 13-Feb-1998 #text_change 21-Ju1-2000 C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Ju1-2000 C; Date: 13-Feb-1998 #te

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A: Accession: S69927
A: Status: nucleic acid sequence not
A: Molecule type: DNA
A: Residues: 1-210 < JAU>
A: Cross-references: EMBL: X69589
A: Experimental source: strain PKa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Borrelia burgdorferi (Lyme disease A, Variety: strain pRa C:Date: 15-reb-1997 #sequence_revision 27-feb-C:Accession: $69927; $72669 R.Jauris-Heipke, S.; Liegl, G.; Preac-Mursic, J. Clin. Microbiol. 33, 1860-1866, 1995 A:Title: Molecular analysis of genes encoding A:Reference number: 140047; MUID:95395018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A; Reference number: $72669
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                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                              17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-May-2000
                                                                                                                   KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 180
                   ELTSPVVAESP
                                                                                           KLKDKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                    IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIEAAKKCSETFTN 136
                                                                                                                                                                                                            IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                           ISCNNSGKDGNTSANSADESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 76
                                                                                                                                                                                                                                                                                                      MACNNSGKDGNTSANSADESVKGFNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKA 60
                                                                                                                                                                                                                                                                                                                                                                                        186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIKEKHTDIGKEGYTDADAKEAIIKTNGTKTKGAEELGKIFESVEVLSKAAKEMIANSVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELTSPVVAESP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGKKIHONNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188;
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.7%;
98.4%;
                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 921; DB 2;
Pred. No. 3.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 928; DB 2;
Pred. No. 1.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          February 1994
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                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V.; Roessler,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 210
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                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.; Schwab, E.; Soutschek,
                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 19-212 <LIV>
A;Cross-references: EMBL:L42883; NID:g858709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain PWudI
A; Note: the nucleotide sequence was submitted to the EMBI
R; Livey, I.; Glbbs, C.P.; Schustevs, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A; Title: Evidence for lateral transfer and recombination
A; Reference number: S70255; MUID:96296448
A; Accession: S70275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-212 <FUC>
A; Residues: 1-212 <FUC>
A; Residues: 1-212 <FUC>
A; Residues: 1-212 <FUC>
A; Cross-references: EMBL:X62162; NID:g39392; PIDN:CAA44093.1; PID:g39393
A; Cross-references: EMBL:X62162; NID:g39392; PIDN:CAA44093.1; PID:g39393
A; Theisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J.; Hansen, K.
A; Theisen, Microbiol. 31, 2570-2576, 193
A; Title: Polymorphism in ospC gene of Borrelia burgdorferi and immunorea.
A; Reference number: I40105; MUID:94075528
A; Recession: I40107
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: DNA
A:Residues: 1-212 <JAU>
A:Cross-references: EMBL:X69590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross references: EMBL:X73624; NID:g313273; PIDN:CAA52003.1; PID:g313274
A;Experimental source: strain DK26
R;Jauris-Heipke, S.; Liegl, G.; Preact-Mursic, V.; Roessler, D.; Schwab, E.; Soutschek
J. Clin. Microbiol. 33, 1860-1866, 1995
A;Title: Molecular analysis of genes encoding outer surface protein C (OspC) of Borre
A;Reference number: 140047; MUID:95395018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer surface protein C precursor - Lyme disease spirochete N;Alternate names: membrane-associated protein pC C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Pate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000 C;Accession: S20543; I40107; S69931; S70275; S34175 R;Fuchs, R.; Jauris, S.; Lottspeich, F.; Preac-Mursic, V.; Wilske, B.; Soutschek, E. Mol. Microbiol. 6, 503-509, 1992 Mol. Microbiol. 6, 503-509, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-205 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession:
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A;Title: Molecular analysis and expression
A;Reference number: S20543; MUID:92219995
A;Accession: S20543
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                                                                                                                                                                                                                                                                                                                                                               Matches 186;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
200
                                        375
                                                                                      140
                                                                                                                                                                                              255 QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 314
                                                                                                                                                                                                                                                                                                                      195
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                                                                     LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
                                                                                                  LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
                                 LGHRNNSGGDSASTNP--DESAKGP 397
                                                                                                                                                                   QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK
                                                                                                                                                                                                                                                          NNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG
                                                                                                                                                                                                                                                                                     SNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyme disease spirochete surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source: strain JSB
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                32.2%;
90.7%;
                                                                                                                                                                                                                                                                                                                                                        Score 886; DB 2;
Pred. No. 1.1e-32;
2; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:AAB36991.1;
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EMBL

Data

Library,

February 1994

immunoreactivity of Os

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OspC

variation in Lyme

PID: g1695209

Length 212;

Indels

14;

Gaps

'n

79

139

В á 밁 Ş В Ş Ъ δÃ

RESULT S37727

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outer surface protein C precursor - Lyme disease spirochete C; Species: Borrella burgdorferi (Lyme disease spirochete) C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000 C; Accession: S37727 R; Jauris-Heipke, S.; Fuchs, R.; Motz, M.; Preac-Mursic, V.; Schwab, E.; Soutschek, Med. Microbiol. Immunol. 182, 37-50, 1993 A; Title: Genetic heterogenity of the genes coding for the outer surface protein C (A; Reference number: S37726; MUID: 93268136 A; Accession: S37727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Jauris-Heipke, S.; Liegl, G.; Preac-Mursic, J. Clin. Microbiol. 33, 1860-1866, 1995
A:Title: Molecular analysis of genes encoding A:Reference number: 140047; MUID:95395018
A:Accession: S69919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer surface protein C precursor - Borrella garinii (strain PTrob) C;Specles: Borrella garinii A;Variety: strain PTrob A;Variety: strain PTrob C;Date: 06-Dec_1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
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A;Residues: 1-207 <JAU>
A;Cross-references: EMBL:x69595; NID:g311393; PIDN:CAA49305.1;
C;Superfamily: Lyme disease spirochete surface protein C
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                                                                                                                                                                                                                                                                       C;Superfamily: Lyme disease spirochete surface protein C F;1-18/Domain: signal sequence #status predicted <SIG> F;19-207/Product: outer surface protein C #status predict
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                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain PTrob
                                                                                                                                                                  Query Match
Best Local S
Matches 180
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Best Local Sim
Matches 181;
                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: nucleic acid sequence not shown; plecule type: DNA esidues: 1-207 <JAU>
                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:X83554; NID:g872027; PIDN:CAA58544.1; PID:g872028
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80
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                                                                                 20
                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 the nucleotide sequence was submitted to the EMBL Data Library, January 1995
                   NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSH
                                                                                                         NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIK 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKEKIKEAKDCSQKFTTKLKDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIK
                                                                                 NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIK
NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKEKIKEAKDCSEKFTTKLKDSH
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                                                                                                                                                                                      31.9%;
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                                                                                                                                                                    2
                                                                                                                                                                                    Score 878; DB 2;
Pred. No. 2.4e-32;
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation not
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.8e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outer surface protein
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                                                                                                                                                                                                                                                                          predicted
                                                                                                                                                                                                          Length 207;
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                                       498
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C;Genetics:
A;Gene: ospC
C;Superfamily:

Lyme

disease spirochete surface

protein

A; Cross-references:

EMBL: X73626; NID: g313277; PIDN: CAA52005.1;

PID: 9313278

from GB/EMBL/DDB

R;Theisen, M.; Frederiksen, B.; Lebech, A.M.; Vuust, J. Clin. Microbiol. 31, 2570-2576, 1993
A;Title: Polymorphism in ospC gene of Borrelia burgda A;Reference number: I40105; MUID:94075528
A;Accession: I40122

burgdorferi

immunoreactivity

of

ت :.

A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-200 <RES>

outer surface protein C - Lyme disease spirochete (strain DK6) (fragment) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-20;C;Accession: I40122; S34177

#text_change 26-May-2000

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outer surface protein C precursor - Borrelia afzelii (strain PBo)
c; Species: Borrelia afzelii
A; Varlety: strain PBo
A; Varlety: strain PBo
C; Date: 06-Dec-1996 #sequence_revision 14-Feb-1997 #text_change 26-May-2000
C; Accession: S69921; 140047
R; Jauris-Helpke, S; Litegl, G; Preac-Mursic, V.; Roessler, D.; Schwab, E.;
J. Clin. Microbiol. 33, 1860-1866, 1995
A; Title: Molecular analysis of genes encoding outer surface protein C (OspC)
A; Reference number: 140047; MUID:95395018
A; Accession: S69921
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-212 <JAU>
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Best Local Sim
Matches 184;
200
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                                                                                                                                               QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 314
L----
                                                                             LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
                              LGHRNNSGGDSASTNP--DESAKGP 397
                                                             LKSGHADLGKQDATDEHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
                                                                                                                              QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK
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                                                                                                                                                                                                                                                                                                                                                 disease
-TSPVVAESPKKP
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                                                                                                                                                                                                                                                                                                                                               spirochete
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Pred.
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                                                                                                                                                                                                                                                                                                                                                 surface
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No. 2.
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C.Species: Borrella afzelii
C.Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #te
C.Accession: I40115; S54187
R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen,
J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrelia burgdorferi outer s
A;Reference number: I40104; MUID:95286481
A; Molecule type: DNA
A; Residues: 1-179 < THE>
                                       A;Accession: I40115
A;Status: translated from GB/EMBL/DDBJ
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A:Title: Evolution of the Borrelia burgdorferi outer s A:Reference number: 140104; MUID:95286481
A:Accession: 140129
                                                                                                                                                                                                                                                                                                                                                                                    В
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C;Superfamily: Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references:
C; Genetics:
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A; Residues: 1-177 < RES>
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Best Local
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Best Local Similarity
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                                                                                                                                                                           Borrelia afzelii (strain DK2) (fragment)
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98.9%;
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Pred. No. 2.5e-31;
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                                                                                 outer surface protein OspC
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                                                                                                             B.; Lebech, A.M.; Hansen,
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A;Residues: 1-179 <THE>
A;Cross-references: EMBL:X84771; NID:g793803; PIDN:CAA59242.1;
A;Experimental source: strain DK3
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: ospC
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: submitted C; Genetics:
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A;Title: Evolution of the Borrella burgdorferi outer surface protein OspC
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S54188
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A; Status: translated from
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C; Date: 08-Jul-1995 #sequen
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Best Local
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Matches
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                                                                                                                                                                                                                                                             262
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                                                                                                                                                                                                                            GLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNKLKSGHAD
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                                                                                                                                                                                                                                                                                                                                              Score 844; DB Pred. No. 6.3e 0; Mismatches
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Pred. No. 5.1e-31;
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                                                                                                                                                                                                                                                                                                                                              nes 1;
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                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                          #text_change 08-Dec-2000
                                                                                        DK8)
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                            B.; Lebech, A.M.; Hansen,
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surface

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A; Molecule type: DNA
A; Residues: 1-180 <THE>
A; Cross-references: EMBL: X84776; NID: g793809; PIDN: CAA59247.1;
A; Note: submitted to the EMBL Data Library, February 1995
C; Genetics:
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C; Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer surface protein C - Borrella afzelii (strain DX21) (fragment)
C;Speckes: Borrella afzelii
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Dec-2000
C;Accession: I40114; S54186
R;Theisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Hans
J. Bacteriol. 177, 3036-3044, 1995
A;Title: Evolution of the Borrella burgdorferi outer surface protein OspC.
A;Reference number: I40104; MUID:95286481
A;Accession: I40114
RESULT 13
570263
couter surface protein C - Lyme disease spirochete (strain C:Species: Borrelia burgdorferi (Lyme disease spirochete) A:Variety: strain KL11
C:Date: 12-Feb-1998 #sequence_revision 26-Feb-1998 #text_c
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A; Residues: 1-179 <THE>
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A; Accession: I40119
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Best Local Similarity
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                                                                                                                                                                                                                GLAALHNQNGSLLAGAYAISTTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNKLKSGHA
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Pred. No. 2.1e-30;
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Pred. No. 1.7e-30;
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     26-Feb-1998 #text_change
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                                                        KL11) (fragment)
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A:Experimental source: strain KL11 R;Livey, I.; Gibbs, C.P.; Schuster, submitted to the EMBL Data Library, A;Reference number: $77616 A;Accession: $77616
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R;Livey, I.; Gibbs, C.P.; Schuster, R.; Dorner, F.
Mol. Microbiol. 18, 257-269, 1995
A;Title: Evidence for lateral transfer and recombination
A;Reference number: S70255; MUID:96296448
A;Accession: S70263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \ensuremath{\mathtt{A}}\xspace; \texttt{Gene: ospC}   
C;Superfamily: Lyme disease spirochete surface protein
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A;Residues: 1-110,'E',112-117,'R',119-189 <LIW>
A;Cross-references: EMBL:L42880; NID:g858707; PIDN:AAB36989.1;
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A;Accession: 140271
A;Status: preliminary; translated
A;Molecule type: DNA
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C;Superfamily: Lyme
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Best Local Similarity
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Residues: 1-207 <RES>
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                                                          NNSGGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEVEALLSSIDELSKAIGKKIK 438
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NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKEKIKEAKDCSEKFTTKLRDSH 139
                              NDGTLDNEANRNESLIAGAYEISKLITQKLSVLNSEELKKKIKEAKDCSQKFTTKLKDSH 498
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Pred. No. 7.
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Pred. No. 1.9e-29;
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C:Species: Borrelia garinii
C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Dec-2000
C:Accession: 140126; S54198
Parheisen, M.; Borre, M.; Mathiesen, M.J.; Mikkelsen, B.; Lebech, A.M.; Hansen, K.
acteriol. 177, 3036-3044, 1995
Talle: Evolution of the Borrelia burgdorferi outer surface protein OspC.
A:Reference number: 140104; MUID:95286481
A:Accession: 140126
Search completed: March 18, 2002, 09:56:49 Job time: 372 sec
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-200 <THE>
A;Cross-references: EMBL:X84781; NID:g793819; PIDN:CAA59252.1; PID:g793820
A;Note: submitted to the EMBL Data Library, February 1995
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C;Superfamily: Lyme disease spirochete surface protein C
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S54198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.9%; Score 794; DB 2; Length 200; Best Local Similarity 89.0%; Pred. No. 1.1e-28; Matches 161; Conservative 13; Mismatches 7; Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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DE PROTEIN C PRECURSOR (PC).
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OUTER SURFACE PROTEIN C.

N-ACYL DIGLYCERIDE (BY SII;

7A4FC978F91777BF CRC64;
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Best Local :
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VM24_BORHE
P32778;
01-OCT-1993
01-OCT-1993
01-FEB-1994
                                                 Bacteria; Spirochaetales;
NCBI_TaxID=140;
                                                                                                                         Plasmid.
                                                                                                                                                                                        VMP24
                                                                                                                                                                                                                     VARIABLE MAJOR
SEQUENCE FROM N.A.
                                                                                                                                                          Borrelia
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J. Clin. Microbiol. 31:2570-2576(1993).
-i- FUNCTION: NOT KNOWN; MAJOR IMMUNODOMINANT PROTEIN.
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MEMBRANE LIPOPROTEIN 2
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Mol. Microbiol. 6:3299-3311(1992).
-I- FUNCTION: SERVES TO AVOID THE HOST IMMUNE FROM ONE SURRACE EXPOSED VMP TO ANOTHER.
                                            SEQUENCE FROM N.A.
STRAIN-SSP. HS1 SEROTYPE 3;
MEDLINE-93133110; PubMed-1484486;
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ProDom; PD001149; Lipoprotein_6; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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"Subtelomeric expression regions of Borrelia hermsii linear plasmids
                                                                                                                                                                                                                               Borrelia
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22541 MW;
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MEMBRANE LIPOPROTEIN 3 PRECURSOR
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PROBABLE.
VARIABLE MAJOR OUTER MEMBRANE
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N-ACYL DIGLYCERIDE
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Pred. No. 4.9e-11;
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of Borrelia herms;
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SPAC1F3.06C.
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Outer membrane; Lipoprotein; Signal; Plasmid SIGNAL 1 18

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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                              Q10411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                             STRAIN=972;
Connor R., Churcher C.
                                                                                                                                      Schizosaccharomyces pombe (Fi
Eukaryota; Fungi; Ascomycota;
Schizosaccharomycetales; Schi
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Microbiol. 6;3299-331(1992).
FUNCTION: SERVES TO AVOID THE HOST IMMUNE RESPONSE FROM ONE SURFACE EXPOSED VMP TO ANOTHER.
SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRAN
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L 222.8 KDA PROTEIN C1F3.06C IN CHROMOSOME
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Bioinformatics Institute.
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cota; Schizosaccharomycetes;
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Pred. No. 7.5e-11;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z70690; CAA94624.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                            336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send
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                                                                                                                                                                  KSKLD---
                                                                                                                                                                                       HGTKDKGAKELEELFKSLESLSKAAQAALTNSVKELTNPV
                                                                                                                                                                                                                                                --EEL---
                                                                                                                                                                                                                                                                  KLSLDLKNLRSSLNVAISDNDQILTQLAELSKNYDSLEQESAQLNSGLKSLEAEKQLLHT
                                                                                                                                                                                                                                                                                                                      QSQNNTLLESESKLKTDCENLTQQNMTL1-----DNVQKLMHKHVNQESKVSELKEVNG
                                                                                                                                                                                                                  ENEELHIRLDKLTGKLKIEESKSSDLGKKLTARQEE
                                                                                                                                                                                                                                                                                             AIGKKIKN-DGTLDNEANRNESLIAGAYEISK----LITQKLSVLNS
                                                                                                                                                                                                                                                                                                                                                --RNNS--GGDSASTNPDESAKGPNLTVISKKITDSNAFLLAVKEV--EALLSSIDELSK
                                                                                                                                                                                                                                                                                                                                                                                                     ILKTHATTDKGAKEFKDLFESVEGL-----LKAAQVALTNSVKELGH-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTLCNAFQEKLAKSVMQLKENEQNFSSLDTSFKKLNESHQELENNHQTITKQLKDTSSKL 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKKHEVYESQLNELKGELQTEI----SNSEHLSSQLSTLAAEKEAAVATNNELSESKNSL 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITDSNAF----VLAVKEVETLVLSIDELAKK--AIGQKIDNNNGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK-EMLANSVKELTSPVVAESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RACLNSSNELKEKSALIDKKDQELNNLREQIKE----QKKVSESTQSSLQSLQRDILNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESV--EVLSK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --YQNNLSSKDKMVKQVSSQLEEARSSLAHATGKLAEINSERD-FQNKKIKDFEKIEQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIHQNN------GLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLK--EKIDA-A 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDSRTSNSQLEEEMVELKESNRT-IHSQLTDAESKLSSFEQENKSLKGSIDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDGNTSANSADE---SVKGPNLTEISKKITDSNAVLLAV-KEVEALLSSIDEIAAKAIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AALNNQNGSLLAGAYAISTLITEKLSKL-----
                                                                                                                                                                                                                                        -KKKIKEAK--DCSQKFTTKLKDSHAELGIQSVQDDN--AKKAILKT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.78; 22.48;
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                                                                                                                                                              ETLSKSSK--LEADIEHLKNKV 999
(Baker's yeast)
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                                                                                              PRT;
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                           PROTEIN USO1
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No. 0.065;
                                       update)
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53

IDETAAKAIGKKIHQNNGLD--TEYNHNGSLLAGAY--

52 984 95

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Matches
                                               Query Match
                                                                                                       CONFLICT
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                        Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF SEQUEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN X2180-1A;
STRAIN X2180-1A;
MEDLINE-91185402; PubMed=2010462;
MEDLINE-91185402; Ogawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-8 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hostetter M.K., Herman
Kendrick K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 782-1790 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; ;
Saccharomycetales;
        Local Sin
nes 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A cytoskeleton-related gene, uso1, protein transport in Saccharomyces of Cell Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamasaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL. SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE
                                                                                                                                                                                                                                                                                                                                                                                                                      ; P80220; 1DIP.
S0002216; USO1.
rPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPI
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FEB-1993)
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1172
847
924
1253
1319
1461
1581
1600
1661
1772
1790
        Conservative
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1319
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1600
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                                                                                                                                                                                                                                                                                                                                                                                                 transport;
                      7.5%;
21.4%;
                                                                                                       206424
                                                                                                                                                                                                                                                                                                                                                                                                                  Spectrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ
        104;
                                                                                                 ASP/GLU-RICH (ACIDIC).

G -> E (IN REF. 2).

E -> K (IN REF. 2).

V -> I (IN REF. 2).

I -> V (IN REF. 2).

I -> V (IN REF. 2).

I -> V (IN REF. 2).

G -> S (IN REF. 2).

G -> S (IN REF. 2).

G -> S (IN REF. 2).

R -> U (IN REF. 2).

R -> U (IN REF. 2).

R -> GCE2B216E9FD4818 CRC
  Score 207.5;
Pred. No. 0.07
04; Mismatches
                                                                                                                                                                                                                                                                                                                     CHARGED (HYPER-HYDROPHILIC)
DISPENSABLE FOR THE PROTEIN
                                                                                                                                                                                                                                                                                                                                                            COILED COIL
                                                                                                                                                                                                                                                                                                                                                                                 GLOBULAR HEAD
                                                                                                                                                                                                                                                                                                                                                                                             Golgi stack; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bendel
                                                                                                     6CE2B216E9FD4818 CRC64;
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                        .079;
                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                         DB
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      259;
                                         1;
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FROM THE ER
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RESULT
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AC QI
DT 0
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-92315338; PubMed-1617731;
Galinski M.R., Medina C.C., Ingravallo P
Galinski M.R., Medina protein complex
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993
01-APR-1993
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RBP1_PLAVB
Q00798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1484
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                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                      -i- FUNCTION: INVOLVED IN RETICULOCYTE AL HUMAN RETICULOCYTE CELLS.
-i- SUBUNIT: HOMODIMER (POTENTIAL).
-i- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
                                                                                                                                                                                                      Cell 69:1213-1226(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BVAJd
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Alveolata;
NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                   RBP1.

Plasmodium vivax (strain Belem).
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(Rel. 25, Last sequence update)
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E BINDING PROTEIN 1 PRECURSOR.
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QNEMSRIN-VEEGSLTDIDKKITD
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                                FKSLESLSKAAQAALTNSVKELTN
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27; Conservative
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SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1
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Pfam; PF00063; myosin_head; 1.
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"Complete nucleotide sequence and deduced polypeptide sequence monamuscle myosin heavy chain gene from Acanthamoeba: evidence chicago in the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87308395;
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28 EISKKITDSNAVLLAVKEVEA----LLSSIDE----IAAKAIGKKIHQNNGLDTEYNH
                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHO CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTARE CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIECE THE REGULATORY PHOSPHORYLATION SITES RESIDE.
MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDITHE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTISIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 2 1Q DOMAINS.
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A27224; A27224.
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                                                                Similarity
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                                            Conservative
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682
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                                                              7.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actin-binding; ATP-binding; Calmodulin-binding; ion; Phosphorylation; Multigene family.

89 MYOSIN HEAD-LIKE.
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                                                            Score
Pred.
                                                                                                                                                                METHYLATION (TRI-) (POTENTIAL)
ALKYLATION (SH-1) (POTENTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                             ACTIN-BINDING.
ACTIN-BINDING.
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NONHELICAL TAILPIECE.
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                                        Mismatches
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                                                              204.5;
No. 0.
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                                                              .086;
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                                          218;
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Q99323;
Q1-JUN-1994
01-JUN-1994
                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropo
Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1415
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MYOSIN HEAV
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Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                 melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                        (Rel. 29, Created)
(Rel. 29, Last sequence up
(Rel. 40, Last annotation
Y CHAIN, NON-MUSCLE (ZIPPER
Swiss Institute of Bioinf
Bioinformatics Institute.
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he myosin tail and differential
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                                                                                                                                                                                                                                                                                Hexapoda;
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        gh a collaboration EMBL outstation -
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Query Match
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VARSPLIC
SEQUENCE
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Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
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NP_BIND
DOMAIN
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InterPro; IPR000048; IQ.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M35012; AAA28713.1; -.
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ELEDATIELEAQRTKVLELEKKQKNFDKILAEEKAISEQIAQERDTAEREAREKE-----
                                                                                         KEFKDLFESVEGLLKAAQ----VALTNSVKELGHRNNSGGDSASTNPDESAKGPNLTVISK
                                                                                                                                      QQLLEEETRQKLGLSSKLRQIESEKEALQEQLEEDDEAKRNYERKLAEVTTQMQEIKKKA
                                                                                                                                                                                                                                                                                                 ESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVK--EVETLVLSID
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                                   KITDSNAFLLA----VKEVEALLSSIDEL---SKAIGKKIKND-GTLDNEANRNESLIAG
                                                                    EEDADLAKELEEGKKRLNKDIEALERQVKELIAQND-----RLDKSKK-----KIQS
                                                                                                                                                                         KKCSEEFT-----
                                                                                                                                                                                                           EKCTK-LQQEAEN-----ITNQLEEAELKASA-----AVKSASNMESQLTEA
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SM00242; MYSc; 1.
'E; PS50096; IQ; 1.
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1 829 MYOSIN
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23.3%;
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25 KDA/50 KDA JUNCTION.

50 KDA/20 KDA JUNCTION.

50 KDA/20 KDA JUNCTION.

ACTIN-BINDING.

REACTIVE SULFHYDRYL/ACTIN-BINDING.

LIGHT MEROMYOSIN (LMM).

ALPHA-HELICAL TAILPIECE (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLOBULAR TAILPIECE.
MISSING (IN SHORT ISOFORM).
MW; 73E3CB02BA8F2528 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agreement (See
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Pred. No. 0.
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| Usage by and for commercial

| http://www.isb-sib.ch/announce/
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MYOSIN II HEAVY CHAIN, NON MUS
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Wagle G., Noegel A., Scheel J., Gerisch G.
"Phosphorylation of threonine residues on
Dictyostellum myosin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Warrick H.M., de Lozanne A., Leinwand L.A., Spudich J.A., "Conserved protein domains in a myosin heavy chain gene f Dictyostelium discoldeum.";
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Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate
"X-ray structure of Dictyostelium discoideum myosin to
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "X-ray structures of the myosin motor domain of Dictyostelium discoideum complexed with MgADP.BeFx and MgADP.AlF4-."; Biochemistry 34:8960-8972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Replacement of threonine residues by phosphorylatable heavy chain fragment FEBS Lett. 269:239-243(1990).
Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.; "X-ray structures of the MgADP, MgATPgammaS, and
                                                                                                        Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II).
"X-ray structure of the magnesium of the magn
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                                        X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
MEDLINE-97452580; PubMed-9305951;
                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE-96206189; PubMed-8611530;
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MEDLINE-95345067; PubMed-7619796;
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MEDLINE-95345066; PubMed-7619795;
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SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
Myosin; Coiled coil; Act
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PDB; 1LVK; 28-JAN-98.
DictyDb; DD01008; mhcA
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J. Mol. Biol. 274.394-407(1997).

-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.

-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKAI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                      Calmodulin-binding; Methylation; DOMAIN 1 761 MYO:
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InterPro; IPR001609; myosin_head.
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ACTIN-BINDING.
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                                                                                                                                                                                               REST_CHICK STANUARA,

042184; 042228; 057563; 057564;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

70-REST_CHICK STANUARA,

15-JUL-1998 (Rel. 36, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

70-REST_CHICK STANUARA,

70-REST_CHICK STANUARA,

6-REST_CHICK STANUARA,

70-REST_CHICK STANUARA,

7
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                           Gallus.
NCBI_TaxID=9031
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                                                                                                     Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1125
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                                                                                                                                                                       gallus (Chicken).
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Pred. No. 0.
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                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                     Galliformes;
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                                                                                                     Phasianidae;
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Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF014012; AAC60344.1; -.
EMBL; AF020764; AAC60345.1; -.
EMBL; AF045550; AAC03547.1; -.
EMBL; AF045651; AAC03548.1; -.
EMBL; AF045651; AAC03548.1; -.
InterPro; IPR000938; CAP-Gly.
InterPro; IPR0001878; Znf_CCHC.
Pfam; PF01302; CAP_GLY; 2.
SMART; SM00343; Znf_C2HC; 1.
PROSITE; PS00845; CAP_GLY_1; 2.
                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griparic L., Keller T.C. III;

"Identification and expression of two novel CLIP-1
expressed predominantly in muscle.";

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ data
-1- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT
THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Pectoralis muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 17-1139 FROM N.A. (CLIP-170(11) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 206:195-208(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griparic L., Volosky J.M., Keller T.C. III; "Cloning and expression of chicken CLIP-170 and restin isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-98137792;
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/
 163
                              826
                                                          118
                                                                                     767
                                                                                                                                             708
                                                                                                                76
                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED CYTOSKELETON (BY SIMILARITY).
ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS
SVEVLSKAAKEMLANSVKELTSPVVAESPAMGSNSGKGGDSASTNPADES - - AKGPNLTE
                              - VNQVKDSLEKELQLLKEKFTSAVDGAENAQRAMQETINKLNQKEEQFALMSSELEQLKS
                                                                                    AALQKANSEGKLEIQKLSEQLQAAEKQIQNLETEKVSNLTKELQGKEQKLLDLEKNLSA-
                                                                                                                   ----NHNG
                                                                                                                                             ESVEDQHLVEMEDTLNKLQEAEIKVKELDVLQAKCNE-QTKLIGSLTQQIRASEEKLLDL
                                                                                                                                                                        ESVKGPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDTEY---
                                                                                                                                                                                                                                                                                                                                                                                                         144
235
305
351
1414
                                                                                                                                                                                                                                                                                                                                   803
458
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microtubules;
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                                                                                                                                                                                                                                                                                                                                                                            121
207
277
277
332
1353
1427
492
492
                                                                                                                                                                                                                 7.0%;
                                                                                                                                                                                                                                                                            161026
                                                                                                                -SLLAGAYAISTLIKQKLDGLKNE--GLKEK-IDAAKKCSET
                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                          170(11+35)).

K -> R (IN F
E -> V (IN F
5631CE86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled coil; Alternative splicing. CAP-GLY 1.
                                                                                                                                                                                                   Score 193; DB
Pred. No. 0.25
98; Mismatches
                                                                                                                                                                                                                                                                                                                                S -> GGSSKVS (IN ISOFORM CLIP-
T -> RKRQISEDPENT (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                              CCHC-BOX.

MISSING (IN SHORT ISOFORM).

TOTKLEHARIKELEQSLLFEKTKADKLORELEDTR ->

RKRQISEDPEN (IN ISOFORM CLIP-170(11)).

S -> GGSSKVS (IN ISOFORM CLIP-170(11)).
                                                                                                                                                                                                                                                                                                                                                                                                                        COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SER-RICH
                                                                                                                                                                                                                                                                          R (IN REF. 2; AAC03547).
V (IN REF. 2; AAC03548).
5631CE8683498E23 CRC64;
                                                         -DAKEAILKTNGTKTKGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel CLIP-170/Restin isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
                                                                                                                                                                                                                    . 25;
                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                      280;
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MENT ASSOCIATED PROTEIN
ULES (BY SIMILARITY).
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                                                                                                                                                                                                                              Length 1433;
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P02566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYOSIN HEAVY CHAIN B (MHC B)
UNC-54 OR MYO-4.
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                                                                                                                   Waterston R.H.;
"The genes sup-7 X and sup-5 III of C. elegans nonsense mutations via altered transfer RNA.";
Cell 33:575-583(1983).
                                                                                                                                                                                                                                        Nature
[3]
                                                                                                                                                                                                                                                       McLachlan A.D., Karn J.;
"Periodic charge distributions in match cross-bridge spacings in mus Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                              myosin
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                                                                                                                                                                                   Wills N., Gesteland
                                                                                                                                                                                                       SEQUENCE OF 1876-1966 FROM N.A. MEDLINE-83232892; PubMed-6571695;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 850-1966 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Rearn J., Brenner S., Barnett L.;

"Protein structural domains in the Caenorhabditis elegans myosin heavy chain gene are not separated by introns.";

Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                                                                                                                                                                                                                                                                                        MEDLINE=82272395; PubMed=7202124;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=83273600; pubMed=6576334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCBI_TaxID=6239;
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FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2),
AND 2 REGULATORY LIGHT CHAIN SUBUNITS OF THE MYOFIBRILS.
SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS, SHOWING
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                       R.F., Karn J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nematoda; Chromadorea;
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                                                                                                                                                                                                                                                                          muscle
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                                                                                                                                                                                       Barnett L.,
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                                                                                                                                                                                                                                                                                                                                                                                                               unc-54
                                                                                                                                                                                                                                                                                            sequence
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MOD_RES
CONFLICT
CONFLICT
SEQUENCE
    1546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY
PRODOM; PD000355; myosin_head; 1.
                                  246
                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REGULTRED FOR MYOSIN ATPASE ACTIVITY.

- I- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT EURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

- I- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C.
                                                                                                                                                 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J01050; AAA28124.1; -. EMBL; V01494; CAA24738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISSP; P08799;
                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                        Match
                         DELAKKAIGQKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAK-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN WALL MISCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAN SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                 VVAESPAMGSNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSI
                                                                                                                              LGKEGVTDADAKEAILKTNGT---KTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSP 185
                                                                                                                                                                     ALDAANSKNASLEKTKSRLVGDLDDAQVDVERANGVASALEKKQKGFDKIIDEWRKKTDD
                                                                                                                                                                                              GLDTEYNHNGSL-LAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTD 128
                                                                                                                                                                                                                                                      SADESVKGPNLTEISKKITDSNAVLLAVK---EVEALLSSIDEI--AAKAIGKKIHQ-NN 69
   -EIEKEELQHALDEAE--AALEAEESKVLRAQVEVS--
                                                                                                            LAAE----LDGAQRDLRNTSTDLFKAKNAQE--ELAEVVEGLRRENKS-LSQEIKDLTDQ 152:
                                                                                                                                                                                                                         SLEEEIEGKN--EILRQLSKANADIQQWKARFEGEGLLKA-DELEDAKRRQAQKINELQE 1414
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                                                                                                                                                                                                                                                                                             127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00242; MYSc;
                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MYSC; 1.
protein; Coiled coil; Thick filament; Actin-binding; ethylation; Alkylation; Multigene family.
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783
128
705
715
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                                                                                                                                                                                                                                                                                                                                                             225125
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                                                                                                                                                                                                                                                                                     Score 192; DB
Pred. No. 0.39
04; Mismatches
                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                     METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGHT MEROMYOSIN (LMM).
ATP (BY SIMILARITY).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL).
ALPHA-HELICAL TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HINGE.
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                                                                                                                                                                                                                                                                                                   DB 1;
.39;
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                                                                                                                                                                                                                                                                                                                Length 1966;
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 QIRSEIEKRI
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RESULT SCAMPLIT SCAMP
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                                    CONFLICT
                                                                                                                  Antigen;
CONFLICT
                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 11-1016 FROM N.A.
Sekeyova Z., Roux V., Raoult D.;
Phylogenetic analysis of Rickettsia spp. by comparing s
'gene D' coding for an intracytoplasmic protein.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCA4_RICPR STANDARD; PRT; 1022 AA. 092D49; 092D48; 09AJ36; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ANTIGENIC HEAT-STABLE 120 KDA PROTEIN (PS120)
                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eriksson A.-S., Winkler "The genome sequence of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _RICPR
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STRAIN=MADRID E;
MEDLINE=99039499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMESHIFT IN POSITION 234.
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AJ235272;
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EFDPL -> RPGLV (IN REF. :)
H -> Y (IN REF. 2).
MISSING (IN REF. 2).
G -> R (IN REF. 2).
0 MW; 03230E3A663A9622 CRC(
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eae; Rickettsia.
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ALT_FRAME.
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Best Local S
Matches 158
                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RESTIN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CL
STERNBERG INTERMEDIATE FILAMENT ASSOCIATED PROTEIN)
                                                                                                                                                                               REST_HUMAN
P30622;
SEQUENCE FROM N.A. TISSUE-Peripheral MEDLINE-92289675;
                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         HOMO
                                                 NCBI_TaxID-9606
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                                                                                                                                                                                                                                                            KAFDNKSSTEE
                                                                                                                                                                                                                                                                                                              APKKVSSLLNDISKRTIEKINNLRAMLS---
                                                                                                                                                                                                                                                                                                                                      LKKKIKE-AKDCSQKFTTKLKDSHAELGIQSVQDDNAKKAILKT-HGTKDKGAKELEELF
                                                                                                                                                                                                                                                                                                                                                                EIQN----LDRELKAQNINESKLHDDIYNKTQDVANALKNVIT---TVLDDNSGQRGVSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTHSDTSLPLHDKVVIMGSVA-----KGIVESKNDLLDRELIIAGLVDGIYE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDSPVQIEMKSKLIQVVTKTVAESALVEPKDKTEIVKG------IGKTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INKQSDLIKEAAIAILNNKKSDFAEKQYNIIDLAKNIFSNKDIIADAKVNVVNTLLETIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KAIGKKIHQNNGLDTEYNHNGSL----LAGAYAISTLIKQKLDGL-----KNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETLYLSIDELAKKAIGQKIDN------NNGL-----AALNNQNGSLLAGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158;
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                                                                                         (Human)
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                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                    544
PubMed=1600942;
                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                  -AKGDNAVVHAISSMIANSN---INQSEKEALKRSQDVVSEKVLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.98;
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Pred.
                                                               Craniata; Vo
Catarrhini;
                                                                                                                                                                                             PRT;
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                                                                                                                                                                                             1427
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                                                                          Vertebrata;
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                                                               Hominidae;
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                                                                          Euteleostomi;
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Best Local S
Matches 135
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DOMAIN
VARSPLIC
CONFLICT
SEQUENCE
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"Restin: a novel intermediate filament-associated protein highly expressed in the Reed-Sternberg cells of Hodgkin's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001878; Znf_CCH(
Pfam; PF01302; CAP_GLY; 2.
SMART; SM00343; ZnF_CZHC; 1.
PROSITE; PS00845; CAP_GLY_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000938; CAP-Gly.
InterPro; IPR001878; Znf_CCHC
Pfam; PF01302; CAP_GLY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES -!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92405160; PubMed=1356075;
Pierre P., Scheel J., Rickard J.E., Kreis T.E.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S22695; S22695
MIM; 179838; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X64838; CAA46050.1; -. EMBL; M97501; AAA35693.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE)
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS
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                                          VIKEKENSLEAIRSKLDKAEDQHLVEMEDTLNKLQEAEIKVKELEVLQAKCNEQTKVIDN
                                                                                                                               KEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAESPAMGSN---
                                                                                                                                                                                           LLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEK-HTDLGKEGVTDADA 139
                                                                                                                                                                                                                        ESNKPAGDVDMSLSLLQEISSLQEKLE-----VTRTDHQREITSLKEHFGAREETHQKE
                                                                                                                                                                                                                                                    EISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLD-----TEYNHNGS
                                                                                                   KVSFSKGLGTETAEFAELKTQIEKMRLDYQHEIENLQNQQDSERAAHAKEMEALRAKLMK
                                                                                                                                                               IKALYTATEKLSKE-----NESLKSKLEHANKENSDVIALWKSKLETAIASHQQAMEEL
                                                                       SGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAK----
                                                                                                                                                                                                                                                                                                 Similarity
KAIGQKI-----
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microtubules; Coiled
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204
279
279
331
1342
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491
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-DNNNGLAALNNQNGSLLAGAYAISTL-----
                                                                                                                                                                                                                                                                                  100;
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                                                                                                                                                                                                                                                                                                                                                                                                    SER-RICH.
COILED COIL
CCHC-BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled coil;
CAP-GLY 1.
SER-RICH.
CAP-GLY 2.
                                                                                                                                                                                                                                                                                                Score 189;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN SHORT ISOFORM).
D -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                           E (IN REF. 2).
OA4F166DD94254E8
                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                   249;
                                                                                                                                                                                                                                                                                                               Length
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                                           750
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               284
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RESULT 15
ZIP1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sym M., Engebrecht J.A., Roeder G.S.;
"ZIP1 is a synaptonemal complex protein required chromosome synapsis.";
Cell 72:365-378(1993).
                                                                                                                                                                                                                                                                       Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Klucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R., Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: REQUIRED FOR MEIOTIC CHROMOSOME SYNAPSIS AND CELL CYCI-PROCRESSION. MAY ACT AS A MOLECULAR ZIPPER TO BRING HOMOLOGOUS CHROMOSOMES IN CLOSE APPOSITION. ZIPI MAY ENCODE THE TRANSVERSE FILAMENTS OF THE SYNAPTONEMAL COMPLEX.
use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way.
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731111;
01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
SYNAPTONEMAL COMPLEX PROTEIN ZIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1074
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                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: SYNAPSED MEIOTIC CHROMOSOMES.
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                                  (See http://www.isb-sib.ch/announce/
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Best Local Similarity 20.1
Matches 115; Conservative
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EMBL; U51031; AAB64474.1;
PIR; A45173; A45173
PIR; S30868; S30868
SGD; S0002693; ZIP1
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DOMAIN
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--LESLEEVTKNLQQKVQSQKRELEQKIKEL
                            KGAKELEELFKSLESLSKAAQAALTNSVKEL 554
                                                       --ELEEQNRHLKNCLEKKETGVEESLSDVKTLKQQVIVLKSEKQDITAEKLELQDN----
                                                                                     SEELKKKIKEAKDCSQKFTTKLKDSHAELGI--QSV-----QDDNAKKAILKTHGTKD 523
                                                                                                                ALVSENDTLKQRIQQLVEIKENEQKDHTTKLEAFQKNNEQLQKLNVEVVQLKAHEL----
                                                                                                                                            ALLSSIDELSKAIGKKI------KNDGTLDNEA--NRNESLIAGAYEISKLITQKLSVLN 472
                                                                                                                                                                          SQISGKEQSLTEKNENLSNELKKVQDQLEKLNNLNITTKSNYENKISSQNEI-----VK
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTSPVVAE
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Pred. No. 0.25;
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2: sp_bacteria
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2750
1 MACNNSGKDGNTSANS
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Match
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Gapop 10.0
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March 18, 2002, 10:10:55; Search time 124.19 Seconds (without alignments) 659.574 Million cell updates/sec
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sp_phage:*
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Q9r7b2
P96507
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Q9S3P3;
01-MAY-2000 (TIEMBLIEL 1:
01-MAY-2000 (TIEMBLIEL 1:
01-JUN-2001 (TIEMBLIEL 1:
01-JUN-2001 (TIEMBLIEL 1:
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NON_TER
SEQUENCE
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                                                                                                                                                                         Mol. Microbiol. 18:257-269(1995).
EMBL; L42887; AAB36995.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                         Livey I., Gibbs C.P., Schuster R., "Evidence for lateral transfer and Lyme disease Borrelia.";
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=IP2;
                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                        MEDLINE=96296448; PubMed=8709845;
                                                                                                                                                                                                                                                                                             NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                         Bacteria;
123
                   61
                                      63
                                                                                                         Local Similarity
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                  KKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKL 122
KEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKEL 182
                                                                                                                                                                                                                                                                                                       Spirochaetales;
                                                                                                                                              192
192 AA;
                                                                                               Conservative
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20287 MW;
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    Created)
    Last sequence update)
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    (FRAGMENT).

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                                                                                                        Score 926;
Pred. No. 3.
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183 180

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60 63

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RESULT
Q9R7B1
ID Q5
AC Q5
DT 0:
DT 0
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Best Local Similarity
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OUTER SURFACE PROTEIN (F

OSPC.
                                                                                                                            P70818;
P70818;
01-FEB-1997
01-FEB-1997
01-JUN-2001
                               Bacteria;
                                                    Borrelia burgdorferi (Lyme
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U91798; AAB81895.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence updat
01-JUN-2001 (TrEMBLrel. 17, Last annotation upd
00TER SURFACE PROTEIN C (FRAGMENT).
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borr
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Ras N.M., Postic D., Foretz M., Baranton G.
"Borrella burgdorferi sensu stricto, a bact
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ilarity 98.4%;
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20297 MW;
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02,
17,
                          Spirochaetaceae;
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Last annotation update)
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Pred. No. 6.6e-35;
2; Mismatches 1
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                                              spirochete)
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Best Local Similarity
                                                                                                                                                                 Matches 184;
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Best Local
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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Wang I.N., Dykhuizen D.E., Qiu W., Dunn
"Genetic diversity of ospC in a local po
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
00TER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probert W.S., Crawford M.R., Cadiz R.B., LeFebvre Submitted (SEP-1996) to the EMBL/GenBank/DDBJ data: EMBL; L81131; AAB06569.1; -. InterPro; IPR001800; Lipoprotein_6. Pfam; PF01441; Lipoprotein_6; 1. Probom; PD001149; Lipoprotein_6; 1. NON_TER 1
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Bacteria; Spirochaet
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF029860; AAB86543.1; -
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STRAIN=2-1498 CA4;
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IGKKIHQNNGLDTEYNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTN 120
                                                 EKHTDLGKEGYTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELT
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186; Conserv
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193 A
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                                                                                                                                                    Score 908; DB 2;
Pred. No. 2.6e-34;
2; Mismatches 1
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Pred. No. 2.1e-34;
""" matches 2;
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RESULT P70818
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Best Local Sim
Matches 181;
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Q9S3P4;
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Bacteria; Spirochaetales;
NCBI_TaxID=139;
                                           01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
OUTER SURFACE PROTEIN C (FRA
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
00TER SURFACE PROTEIN C PRECURSOR (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13,
    Borrelia
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  (Lyme
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    disease spirochete)
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ກຳ. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3e-33;
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on update)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            MEDLINE=97478003: PubMed=9336916;
Ras N.M., Postic D., Foretz M., Bu
"Borrelia burgdorferi sensu strict
U.S.A.'?";
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NON_TER
SEQUENCE
                                           InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
NON_TER 1
NON_TER 182
SEQUENCE 182 AA; 19202 MW; 4221
                                                                                                                                                                      STRAIN-TETS;
Marti-Ras N., Postic D., I
Submitted (MAR-1997) to tl
EMBL; U91797; AAB81894.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
0UTER SURFACE PROTEIN C (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9R7B2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     васteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9R7B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-JSB;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          Int. J. Syst.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-TETS;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fam; PF01441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L42883; AAB36991.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Livey I., Gibbs C.P., Schuster R., 
"Evidence for lateral transfer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Livey I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96296448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVLAVKEVETLVLSIDELAKKAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease Borrelia."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGHRNNSGGDSASTNP--DESAKGP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001800; Lipoprotein_6.
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194 i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                          Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein_6; 1.
49; Lipoprotein_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18:257-269(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8709845;
                                  182
19202 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSPVVAESPKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
20446 MW;
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                                                                                                                                                                                                                                                                                                          47:1112-1117(1997)
                                                                                                                                                                                                                        Foretz M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spirochaetaceae; Borr
                                                                                                                                                                                                                                                                                                                                                   M., Baranton G. stricto, a bact
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                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEEDC9FA5DF0D68F CRC64;
                                               422146F99AA57BF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    886;
No. 2.
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                                                                                                                                                                                                                        Baranton
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masuzawa T., Sawaki K., Yoshii T.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AB000345; BAA19078.1;
EMBL; AB009895; BAA24125.1;
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Masuzawa T., Komikado
Submitted (JAN-1997) t
                                                     194
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Bacteria; Spiroch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0UTER SURFACE PROTEIN C (FRAGMENT).
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                                                                                                                                                                                                                                                                      255
                                                                                                                                                                                                                                                                                                  Bacteria; Spirochaetales;
NCBI_TaxID=29518;
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ι.
                                                                                                                                                                                                             QKIDNNNGLAALNNQNGSLLAGAYAISTLITEKLSKLKNLEELKTEIAKAKKCSEEFTNK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKSGHADLGKQDATDDHAKAAILKTHATTDKGAKEFKDLFESVEGLLKAAQVALTNSVKE 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 32.18; ilarity 99.48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203
21549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to 1:,
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99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Fukui T., Yanagihara
the EMBL/GenBank/DDBJ (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                              Score 884; DB 2;
Pred. No. 3.3e-33;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94A885FBBACFE1C4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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.6e-33;
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Wilske B., Preace-Mursic V., Jauris S., Pradel I., Sout. Schwab E., Wanner G.;

"Immunological and molecular polymorphisms of OspC, an major outer surface protein of Borrelia burgdorferi.";

Infect. Immun. 61:2182-2191(1993).

EMBL; X69595; CAA49305.1;
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InterPro; IPR001800; Lipoprotein_6.

Pfam; PR01441; Lipoprotein_6; 1.

ProDom; PD001149; Lipoprotein_6; 1.

SEQUENCE 207 AA; 22320 MW; 4A525ABDAE63B5C8 CRC64;
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Jauris-Heipke S., Fuchs R., Motz M., Preac-Murs
Will G., Wilske B.;
"Genetic heterogenity of the genes coding for t
protein C (OspC) and the flagellin of Borrelia
Med. Microbiol. Immunol. 182:37-50(1993).
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Spirochaetaceae;
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Best Local Similarity
Matches 185; Conserv
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01-NOV-1996
01-JUN-2001
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ database: EMBL; AF730185; AAF75626.1;
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
Probom; PD001149; Lipoprotein_6; 1.
SEQUENCE 212 AA; 22495 MW; C51DAF803BF2E7D4 CRC64;
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Q45187;
                                                                                                   Jauris-Heipke S., Liegl G., Preac-Mursic V., Roessle Soutschek E., Will G., Wilske B.; "Molecular analysis of genes encoding outer surface of Borreila burgdorferi sensu lato: relationship to evidence of lateral gene exchange of ospC."; J. Clin. Microbiol. 33:1860-1866(1995).
                                                                                                                                                                                                                                MEDLINE-9521333; pubMed-7699024; Wilske B., Jauris-Helpke S., Lobentanzer R., Pradel I., Wilske B., Jauris-Helpke S., Lobentanzer R., Pradel I., Pradel I., Soutschek E., Johnson R.C.; "Phenotypic analysis of outer surface protein C (OspC) of Borrelia burgdorferi sensu lato by monoclonal antibodies: relationship to genospecies and OspA serotype."; J. Clin. Microbiol. 33:103-109(1995).
STRAIN-PSCF, PBAEII, PFIN, PFLK, PMUE, PSH;
Marconi R.T., Hohenberger S., Jauris-Heipke S., Schulte-Spechtel L
Lavole C.P., Roessler D., Wilske B.;
"Genetic analysis of B.garinii OspA-serotype 4 strains associated
neuroborreliosis: evidence for extensive genetic homogeneity.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            Borrelia garinii.
Bacteria; Spirochaetales;
NCBI_TaxID=29519;
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MEDLINE-95395018; PubMed-7665660;
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Pred. No. 5.2e
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EMBL; AJ132793; CAB46231.1; -.
EMBL; AJ132796; CAB46234.1; -.
EMBL; AJ132797; CAB46235.1; -.
EMBL; AJ132798; CAB46235.1; -.
EMBL; AJ132798; CAB46236.1; -.
EMBL; AJ236907; CAB46237.1; -.
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LaVole C.P., Roessler D., Wilske B.;
"Genetic analysis of Borrelia garinii OspA
associated with neuroborreliosis evidence
                                                                                                                                                                                                                                                                Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
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NCBI_TaxID=29519;
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EMBL; AJ123795; CAB46233.1; -
InterPro; IPR001800; Lipoprotein_6.
Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 207 AA; 22249 MW; 20889AA7.
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Bacteria; Spirochaetales;
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD0001149; Lipoprotein_6; 1.
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Pfam; PF01441; Lipoprotein_6; 1.
ProDom; PD001149; Lipoprotein_6; 1.
SEQUENCE 212 AA; 22514 MW; C6EDC33BFD488DDE
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"Molecular analysis of genes encoding outer surfa of Borrelia burgdorferi sensu lato: relationship evidence of lateral gene exchange of ospC.";
J. Clin. Microbiol. 33:1860-1866(1995).
EMBL; X81521; CAA57241.1;
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